

**GENETIC CONSTRUCTS HAVING HETEROLOGOUS 3'
POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT
FUNCTION IN PLANTS**

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CROSS-REFERENCE TO RELATED APPLICATIONS

[01] This application claims the benefit under 35 U.S.C. § 119(e) of U.S.S.N. 60/390,529, filed June 20, 2002, which is incorporated herein in its entirety.

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whatsoever.

FIELD OF THE INVENTION

[03] The present invention relates to heterologous genetic constructs comprising non-plant 3' termination sequences and plant expression cassettes incorporating the heterologous genetic constructs. The present invention also comprises methods for construction of the plant expression cassettes and introducing the cassettes into plant cells.

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BACKGROUND OF THE INVENTION

[04] Processing of messenger RNA 3' termination sequences resulting in polyadenylation is a universal feature of gene expression in eukaryotic organisms (See for example, Nevins, J.R.: "The pathway of eukaryotic mRNA formation", *Ann. Rev. Biochem.*, **52**:441-466 (1983)). This type of processing also has profound effects on gene expression, including total cessation of mRNA translation, as both mRNA stability and translatability are linked to polyadenylation. (Wickens, M., *et al.*, "Life and Death in the Cytoplasm: Messages from the 3' termination sequence", *Curr. Opin. Genet. Dev.*, **7**:220-232 (1997)). Evidence is accumulating that such alterations in 3' termination sequence processing represents a form of

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expressional control which is directed by the interaction of trans-factors with cis-elements found in the precursor mRNA 3' termination sequences.

[05] Understanding the role of 3' termination sequence processing in gene expression becomes critical when considering methods of expressing heterologous genes comprising
5 "foreign" 3' termination sequences. This is especially true in the case of plants where the introduction of foreign genes makes dramatic improvements in crop plants feasible through otherwise straightforward gene transfer technology. However, despite extensive research, attempts to express foreign genes with non-plant 3' termination sequences in plants has thus far met with failure. For example, plant cells have been reported to be unable to recognize 3'
10 termination sequences in *Saccharomyces cerevisiae* genes (see e.g.; Barton, K.A., *et al.*, *Cell*, 32:1033-1043 (1983) and Irniger, s., *et al.*, "Different Sequence Elements are required for function of Califlower Mosaic Virus Polyadenylation Site in *Saccharomyces cerevisiae* Compared with in Plants", *Mol. and Cell. Biol.*, 2322-2330 (1992)), as well as many other sources (See e.g., Koncz, c. *et al.*, "A simple method to transfer, integrate and study
15 expression of foreign genes, such as chicken ovalbumin and α -actin in plant tumors", *EMBO J.*, 3:5), 1029-1037 (1984)).

[06] This apparent lack of functionality of foreign 3' termination sequences in plants has lead to a scarcity of 3' termination sequences suitable for use in plant expression vectors for heterologous genes. In effect, only plant and plant viral 3' termination sequences can
20 currently be considered for use in such vectors and, of the possible functional 3' termination sequences, only a few have been developed due to the difficulties in operably linking heterologous sequences to form a functional gene. Still other plant 3' termination sequences are unsuitable as they lead to undesirable recombination events with native sequences or trigger "gene silencing" through various mechanisms such as the formation of anti-sense
25 RNA species. This set of circumstances increases the complexity of expressing foreign genes in plant cells and severely limits a primary method of controlling genetic expression in response to tissue type, environmental stimuli, and other factors. Identification of non-plant 3' termination sequences which are functional in plants, 3' cis regulatory elements necessary for expression in plants, and methods for constructing novel 3' termination sequences capable
30 of functioning in plants would therefore be a significant advance in the expression of foreign genes in plant species.

SUMMARY OF THE INVENTION

[07] The present invention provides recombinant expression cassettes comprising a plant promoter operably linked to a coding sequence having a stop codon and a non-plant 3' termination sequence. The non-plant 3' termination sequence is heterologous to the coding sequence. The non-plant 3' termination sequence also comprises a cleavage site, a positioning element, and an upstream element and has at least 60% identity to a native fungal or native animal 3' termination sequence and less than 90% identity to a native plant 3' termination sequence. Alternatively, the non-plant 3' termination sequence is unable to selectively bind to any known plant sequence under stringent conditions, as defined herein. The cleavage site of the non-plant 3' termination sequence comprises the sequence YA, defining the position of endonucleolytic cleavage and subsequent 3' polyadenylation. The positioning element is 6 bases long, with at least 4 out of 6 bases being adenine, and located between 10 bases and 40 bases 5' of the cleavage site. The upstream element is located between 1 base and 250 bases 5' of the positioning element; and, comprises the sequence TAYRTA or two or more repeats of TA, TG, or TA and TG where the repeats are separated by 0 to 10 bases.

[08] In one aspect of the present invention is a plant cell comprising the expression cassette described in the previous paragraph.

[09] Another aspect of the present invention provides a recombinant expression cassette with a cleavage site flanked by a pair thymidine-rich regions. Each of the thymidine-rich regions comprises at least 6 base pairs of at least 80% thymidine; and is within about 50 bases of the cleavage site.

[10] In another aspect of the invention, the recombinant expression cassette has a viral promoter.

[11] In another aspect, the 3' termination sequence of the recombinant expression cassette has at least 70% sequence identity to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, or SEQ ID NO:31.

[12] A further embodiment of the present invention is an isolated 3' termination sequence that is functional in plants and can be PCR-amplified by primers selectively hybridizing under stringent conditions to the same sequence as either primer pair SEQ ID NOs: 4 and 5, SEQ ID NOs: 6 and 7, SEQ ID NOs: 8 and 9, SEQ ID NOs: 10 and 11, SEQ ID NOs: 32 and 33, SEQ ID NOs: 34 and 35, SEQ ID NOs: 36 and 37, SEQ ID NOs: 38 and 39, SEQ ID NOs: 40 and 41, SEQ ID NOs: 42 and 43, SEQ ID NOs: 44 and 45, SEQ ID NOs: 46 and 47,

SEQ ID NOs: 48 and 49, SEQ ID NOs: 50 and 51, SEQ ID NOs: 52 and 53, SEQ ID NOs: 54 and 55, SEQ ID NOs: 56 and 57, SEQ ID NOs: 58 and 59, or SEQ ID NOs: 60 and 61. In addition, the isolated 3' termination sequence is a nucleotide sequence having at least 60% identity to a native fungal or native animal 3' termination sequence and less than 90% identity to a native plant 3' termination sequence.

[13] Another embodiment of the present invention is a method for isolating a recombinant protein. The method involves obtaining a nucleic acid encoding the recombinant protein, using this nucleic acid in constructing a recombinant expression cassette comprising the nucleic acid and a stop codon, operably linked with a non-plant 3' termination sequence. The non-plant 3' termination sequence used in constructing the expression cassette is heterologous to the coding sequence and comprises a cleavage site, a positioning element, and an upstream element and has at least 60% identity, sometimes at least 70% identity, occasionally at least 80% identity, or possibly at least 90% identity to a native fungal or native animal 3' termination sequence and less than 90% identity to a native plant 3' termination sequence. The cleavage site of the non-plant 3' termination sequence comprises the sequence YA, defining the position of endonucleolytic cleavage and subsequent 3' polyadenylation. The positioning element is 6 bases long, with at least 4 out of 6 bases being adenine, and located between 10 bases and 40 bases 5' of the cleavage site. The upstream element is located between 1 base and 250 bases 5' of the positioning element; and, comprises the sequence TAYRTA or two or more repeats of TA, TG, or TA and TG where the repeats are separated by 0 to 10 bases. The expression cassette is then used to transfect a plant cell. The transfected plant cell is then cultured in a manner allowing the cell to express the recombinant protein. Finally, the recombinant protein is isolated.

[14] Still another embodiment of the invention is a method of identifying non-plant 3' termination sequences that are functional in plants. The method comprises obtaining a non-plant 3' termination sequence that has a nucleotide sequence having at least 60% identity, sometimes at least 70% identity, occasionally at least 80% identity, or possibly at least 90% identity to a native fungal or native animal 3' termination sequence and less than 90% identity to a native plant 3' termination sequence; a cleavage site comprising the sequence YA defining the position of endonucleolytic cleavage and subsequent 3' polyadenylation; a positioning element of 6 bases located between 10 bases and 40 bases 5' of the cleavage site and with at least 4 out of 6 bases being adenine; and an upstream element that is located between 1 base and 250 bases 5' of the positioning element and comprises TAYRTA or two or more repeats of TA, TG, or TA and TG where the repeats are separated by 0 to 10 bases.

This non-plant 3' termination sequence is used in constructing an expression cassette having a functional plant promoter operably linked with a coding sequence encoding a selectable marker that is in turn operably linked with the 3' termination sequence described above. Finally, the selectable trait displayed by the marker gene is detected.

- 5 [15] Another embodiment is a method for making a transgenic plant. The method involves first obtaining a nucleic acid encoding a genetic trait to be expressed. A recombinant expression vector is constructed for the plant transfection. This recombinant expression vector comprises a promoter that is functional in plants operably linked with the nucleic acid encoding the genetic trait to be expressed. The nucleic acid is in turn operably linked with a
- 10 non-plant 3' termination sequence having the same characteristics as the 3' termination sequence described in the previous paragraph. A plant cell is transfected with this recombinant expression vector and is subsequently cultured into a viable plant expressing the genetic trait.
- [16] A further embodiment of the present invention is an isolated 3' termination sequence
- 15 that is functional in plants and is identical to a native fungal or native animal 3' termination sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

- [17] Fig 1 illustrates the functionality of various yeast 3' termination sequences in plants
- 20 by measuring the activity of the linked GUS gene in *Agrobacterium*-infiltrated *Nicotiana benthamiana* leaves.
- [18] Fig 2 illustrates the functionality of various yeast 3' termination sequences in plants by measuring the level of kanamycin resistance in transfected tobacco hairy roots.
- [19] Fig 3 illustrates the functionality of various yeast 3' termination sequences in plants
- 25 by measuring the level of kanamycin resistance in tobacco shoots.
- [20] Fig 4 is a cartoon of composite sequences and a schematic depiction of the relative orientation of cis regulatory sequences in the 3' termination sequences of genes from yeast, plants and animals, respectively.

30 DEFINITIONS

- [21] The term "3' termination sequence" refers to the DNA sequence portion of a gene that contains a polyadenylation signal and any other regulatory signal capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by

affecting an endonucleic cleavage at a "cleavage site" and the addition of polyadenylic acid tracts to the new 3' end created by the cleavage reaction.

[22] The term "3' polyadenylation" refers to the process of adding a string of several to dozens of adenyl residues to the 3' end of a nucleic acid. 3' polyadenylation normally occurs in the course of mRNA processing in the nucleus, following endonucleolytic cleavage of the 3' termination sequence.

[23] The term "cis element" refers to any polynucleotide sequence or region capable of being recognized and bound in a specific manner by a binding partner, usually a protein or nucleic acid.

[24] The term "cleavage site" refers to the nucleotide sequence "YA", and is commonly found flanked by thymidine-rich regions within about 50 nucleotides. Functionally, the cleavage site marks the precise position where the 3' termination sequence processing complex cleaves the 3' termination sequence in preparation for 3' polyadenylation of the freshly formed 3' end. Cleavage at the cleavage site normally occurs between the nucleotide pair making up the cleavage site.

[25] The term "coding sequence", in relation to nucleic acid sequences, refers to a plurality of contiguous sets of three nucleotides, termed codons, each codon corresponding to an amino acid as translated by biochemical factors according to the universal genetic code, the entire sequence coding for an expressed protein, or an antisense strand that inhibits expression of a protein. A "genetic coding sequence" is a coding sequence where the contiguous codons are intermittently interrupted by non-coding intervening sequences, or "introns." During mRNA processing intron sequences are removed, restoring the contiguous codon sequence encoding the protein or anti-sense strand.

[26] The term "expression", as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of the target protein. "Overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms. "Co-suppression" refers to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar foreign or endogenous genes (U.S. Pat. No. 5,231,020, incorporated herein by reference).

[27] The term "endonucleolytic cleavage" refers to severing of the covalent bond between two nucleotides in a polynucleotide chain, neither of the nucleotides being a terminal

nucleotide prior to severing the covalent bond. A terminal nucleotide is a nucleotide that has flanking nucleotides at only its 3' or the 5' end.

[28] The term "functional in plants" refers to the ability of any genetic element or protein to exhibit at least a part of its native behavior in plants. Native behavior refers to those aspects of function normally displayed when expressed or present in a homologous (native) system. When the behavior can be manifested as a measurable activity, the magnitude of the activity can be greater than, equal to or less than the magnitude displayed in a homologous system. Where a genetic element or protein has multiple behavioral aspects, the genetic element or protein is considered "functional in plants" if only one aspect of its native behavior is exhibited to any degree when expressed or present in a plant.

[29] The term "genetic trait" refers to a property of a cell that is encoded in the nucleic acid pool of the cell and normally can be passed on, typically through mitotic or meiotic division, to progeny of the original cell.

[30] The term "heterologous" when used with reference to portions of a nucleic acid or protein indicates that the molecule comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, a heterologous nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

[31] The term "isolate" in all of its grammatical forms refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other components normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

[32] "Nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl

ribonucleotides, peptide-nucleic acids (PNAs). Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by

5 generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner *et al.*, *Nucleic Acid Res.*, **19**:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, **260**:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, **8**:91-98 (1994)). The term "nucleic acid" is used interchangeably with the terms "gene", "cDNA", "mRNA", "oligonucleotide", and "polynucleotide".

10 [33] A particular nucleic acid sequence also implicitly encompasses "splice variants." Similarly, a particular protein encoded by a nucleic acid implicitly encompasses any protein encoded by a splice variant of that nucleic acid. "Splice variants," as the name suggests, are products of alternative splicing of a gene. After transcription, an initial nucleic acid transcript may be spliced such that different (alternate) nucleic acid splice products encode different

15 polypeptides. Mechanisms for the production of splice variants vary, but include alternate splicing of exons. Alternate polypeptides derived from the same nucleic acid by read-through transcription are also encompassed by this definition. Any products of a splicing reaction, including recombinant forms of the splice products, are included in this definition.

[34] As used herein a "nucleic acid probe" or "oligonucleotide probe" is defined as a

20 nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, U, or T) or modified bases (e.g., 7-deazaguanosine, inosine, *etc.*). In addition, a linkage other than a phosphodiester bond may join the bases in a probe, so long as it does not interfere with

25 hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence, depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes,

30 chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

[35] A "labeled nucleic acid probe" or "labeled oligonucleotide probe" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through

ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

[36] The term “nucleotide” refers to a single purine or pyrimidine-derived ribonucleic acid, phosphorylated at least in one position. Unless otherwise indicated, all nucleotide

5 representations in this manuscript comply with the single letter code recommended by the IUPAC-IUB Biochemical Nomenclature Commission, and published by the Patent and trademark Office of the United States in the PatentIn User Manual. These include those for pyrimidines (Y), purines (R), amino (M), keto (K), strong interactions (i.e., G or C) (S), weak interactions (i.e., A or T) (W) and others, in addition to the commonly used symbols A, C, G,
10 T, and U.

[37] The term “nucleotide sequence” refers to a contiguous chain of covalently linked nucleotides.

[38] The term “native fungal” refers to any aspect of a fungus, or portion thereof, that represents the aspect or portion as it occurs naturally in the fungus, but not including variant
15 forms, to any degree, of the aspect or aspect portion.

[39] The term “native animal” refers to any aspect of a animal, or portion thereof, that represents the aspect or portion as it occurs naturally in the animal, but not including variant forms, to any degree, of the aspect or aspect portion.

[40] The term “non-plant”, in relation to isolated biological material, refers to a biological
20 source incapable of undergoing photosynthesis under any circumstances. In relation to synthetic or semi-synthetic material, the term “non-plant” refers to any composition that is not identical to a composition found in plants. For example, a “non-plant 3’ termination sequence” is any 3’ termination sequence that is not identical in nucleotide sequence to a 3’ termination sequence known to exist in any plant or plant pathogen that inserts its DNA into
25 the plant (e.g. Agrobacterium, plant viruses). In the context of this definition, the term “plants” encompasses the organisms classified in the Kingdom Plantae while excluding members of the Kingdom Animalia and the Kingdom Fungi.

[41] The term “operably linked” refers to the association of two or more nucleic acid fragments on a single nucleic acid fragment so that the function of one is affected by the
30 other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

[42] The terms "primers" or "primer pairs" refer to oligonucleotide probes capable of recognizing and hybridizing to specific nucleotide sequences found in a target gene or sequence to be amplified by polymerase chain reaction (PCR). The degree of complementarity required between the primers and the target sequence determines the specificity, or stringency of conditions required for hybridization of the sequences. A temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y. (1990)).

[43] The term "promoter" refers to a nucleotide sequence capable of controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a nucleotide sequence that can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a promoter. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic nucleotide segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. Promoters that cause a nucleic acid fragment to be expressed in most cell types at most times are commonly referred to as "constitutive promoters". New promoters of various types useful in plant cells are constantly being discovered; numerous examples may be found in the compilation by Okamuro and Goldberg, *Biochemistry of Plants*, 15:1-82 (1989). It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, nucleic acid fragments of different lengths may have identical promoter activity.

[44] The term "recombinant DNA" refers to DNA that has been derived or isolated from any source that may be subsequently chemically altered, and later introduced into a plant cell. An example of recombinant DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering.

[45] Therefore "recombinant DNA" includes completely synthetic DNA, semi-synthetic DNA, DNA isolated from biological sources, and DNA derived from introduced RNA. Generally, the recombinant DNA is not originally resident in the plant genotype which is the recipient of the DNA, but it is within the scope of the invention to isolate a gene from a given plant genotype, and to subsequently introduce multiple copies of the gene into the same genotype, e.g., to enhance production of a given gene product such as a storage protein.

[46] The recombinant DNA used for transformation herein may be circular or linear, double-stranded or single-stranded. Generally, the DNA is in the form of chimeric DNA, such as plasmid DNA, which can also contain coding regions flanked by regulatory sequences that promote the expression of the recombinant DNA present in the resultant plant. For example, the recombinant DNA may itself comprise or consist of a promoter that is active in plants, or may utilize a promoter already present in the plant genotype that is the transformation target.

[47] A "recombinant expression cassette" is a recombinant DNA containing a nucleic acid capable of being transcribed in a cell. The recombinant expression cassettes of the invention generally comprise a coding sequence transcribed by cellular (or cellularly-derived) agents, although vectors used for the amplification of nucleotide sequences (both coding and non-coding) are also encompassed by the definition. In addition to the coding sequence, expression vectors will generally include restriction enzyme cleavage sites and the other initial, terminal and intermediate DNA sequences that are usually employed in vectors to facilitate their construction and use. The expression vector can be part of a plasmid, virus, or a nucleic acid fragment.

[48] The term "messenger RNA (mRNA)" refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a double-stranded DNA that is complementary to and derived from mRNA. "Sense" RNA refers to RNA transcript that includes the mRNA. "Antisense RNA" refers to a RNA transcript that is complementary to all

or part of a target primary transcript or mRNA and that blocks the expression of a target gene by interfering with the processing, transport and/or translation of its primary transcript or mRNA. The complementarity of an antisense RNA may be with any part of the specific gene transcript, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding
5 sequence. In addition, as used herein, antisense RNA may contain regions of ribozyme sequences that increase the efficacy of antisense RNA to block gene expression.

[49] The term "plant" refers to a photosynthetic organism, either eukaryotic or prokaryotic. The term "higher plant" refers to a eukaryotic plant. "Native plant" refers to any aspect of a plant, or portion thereof, that represents the aspect or portion as it occurs naturally in the
10 plant, but not including variant forms, to any degree, of the aspect or aspect portion.

[50] The term "positioning element" refers to a region of nucleotide sequence that is 6 nucleotides long, 4 of the 6 nucleotides being adenine, and located between 10 nucleotides and 40 nucleotides upstream of the 3' termination sequence cleavage site. Functionally, the positioning element is believed to be a critical component necessary for correct alignment of
15 the 3' termination sequence processing complex prior to the complex cleaving the 3' termination sequence precisely at the cleavage site, as defined herein.

[51] The terms "selectable marker", or "selectable trait" refers to a molecule that imparts a distinct phenotype to cells expressing the nucleic acid fragment encoding the marker and thus allow such transformed cells to be distinguished from cells that do not have the marker. A
20 selectable marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like). A screenable marker confers a trait which one can identify through observation or testing, i.e., by 'screening'. A "scoreable marker" is a screenable marker with a phenotypic trait that can be quantified.

[52] The phrase "selectively (or specifically) hybridizing" refers to the binding, duplexing, or hybridizing between two particular nucleotide sequences under stringent hybridization
25 conditions when the sequences are present in a complex mixture (e.g., total cellular or library DNA or RNA).

[53] The term "recombinant protein" refers to a protein or polypeptide having a heterologous sequence, the combination of amino acids not normally being present in nature.
30 Recombinant protein also refers to proteins or polypeptides that are transcribed from recombinant (heterologous) genes.

[54] The terms "sequence similarity", "sequence identity", or "percent identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are, when optimally aligned with appropriate nucleotide

insertions or deletions, the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., 50% identity, 65%, 70%, 75%, 80%, preferably 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher identity to a nucleotide sequence such as SEQ ID NO:1), when compared and aligned for maximum correspondence
5 over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition also refers to the complement of a test sequence. Preferably, the identity exists over a region that is at least about 25 nucleotides in length, or more preferably over a region that is 50-100 nucleotides in length. These relationships hold, notwithstanding evolutionary
10 origin (Reeck *et al.*, *Cell*, 50:667 (1987)). When the sequence identity of a pair of polynucleotides or polypeptides is greater or equal to 65%, the sequences are said to be "substantially identical."

[55] The term "stop (or "termination") codon" refers to a unit of three adjacent nucleotides in a polynucleotide coding sequence that specifies translational termination of protein
15 synthesis (i.e., mRNA translation) by the ribosomal complex.

[56] The phrase "stringent conditions" or "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences
20 hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic
25 strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion
30 concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For high stringency hybridization, a positive signal

is at least two times background, preferably 10 times background hybridization. Exemplary high stringency or stringent hybridization conditions include: 50% formamide, 5x SSC and 1% SDS incubated at 42° C or 5x SSC and 1% SDS incubated at 65°C, with a wash in 0.2x SSC and 0.1% SDS at 65°C.

5 [57] The terms "substantially similar" or "substantially identical" refers to nucleic acid fragments wherein changes in one or more nucleotide bases results in substitution of one or more amino acids, but do not affect the functional properties of the polypeptide encoded by the nucleotide sequence. "Substantially similar" also refers to nucleic acid fragments wherein changes in one or more nucleotide bases does not affect the ability of the nucleic acid
10 fragment to regulate gene expression through effects on transcription and translation rates or to mediate gene silencing through for example antisense or co-suppression technology. "Substantially similar" also refers to modifications of the nucleic acid fragments of the instant invention such as deletion or insertion of one or more nucleotides that do not substantially affect the functional properties of the resulting transcript such as 3' end processing, transport,
15 mRNA stability, or the ability to mediate or suppress gene silencing. For "regulatory" or non-coding sequences such as promoters, enhancers, introns, and 3' ends, any of these modifications (base substitutions, insertions, or deletions) that do not significantly affect the functional properties of the sequence would be considered to produce a "substantially similar" nucleic acid. It is therefore understood that the invention encompasses more than
20 the specific exemplary nucleotide or amino acid sequences and includes functional equivalents thereof.

[58] For example, it is well known in the art that antisense suppression and co-suppression of gene expression may be accomplished using nucleic acid fragments representing less than the entire coding region of a gene, and by nucleic acid fragments that do not share 100%
25 sequence identity with the gene to be suppressed. Moreover, alterations in a nucleic acid fragment which result in the production of a chemically equivalent amino acid at a given site, but do not effect the functional properties of the encoded polypeptide, are well known in the art. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more
30 hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a functionally equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal portions of the polypeptide molecule would also

not be expected to alter the activity of the polypeptide. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products.

5 [59] Moreover, substantially similar nucleic acid fragments may also be characterized by their ability to hybridize, under stringent conditions (0.1xSSC, 0.1% SDS, 65 °C), with the nucleic acid fragments disclosed herein.

10 [60] A “comparison window”, as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 4 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.*, 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.*, 15 48:443 (1970), by the search for similarity method of Pearson and Lipman, *Proc. Nat’l. Acad. Sci. USA*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 20 supplement)).

[61] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program 25 parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters. For sequence comparison of nucleic acid sequences, the BLAST and BLAST 2.0 algorithms and the default parameters discussed below are used.

30 [62] The BLAST and BLAST 2.0 algorithms are described in Altschul *et al.*, *Nuc. Acids Res.*, 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.*, 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short

words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing

5 them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each

10 direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences)

15 uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, *Proc. Natl. Acad. Sci. USA*, **89**:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

20 [63] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul, *Proc. Nat'l. Acad. Sci. USA*, **90**:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)). P(N) provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid

25 is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

[64] An alternative to the BLAST program is the GCG (Genetics Computer Group, Program Manual for the GCG Package, Version 7, Madison, Wis.) PILEUP program.

30 PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pair wise alignments to show relationship and percent sequence identity. It also plots a tree or dendrogram showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng and Doolittle, *J. Mol. Evol.*, **35**:351-360 (1987). The method used is similar to the method described by

Higgins and Sharp, *CABIOS*, 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pair wise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related
5 sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pair wise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pair wise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. For example, a reference sequence
10 can be compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps.

[65] The terms "thymidine-rich or T-rich region" refer to a region of nucleotide sequence at least 6 nucleotides long, within about 50 nucleotides of the 3' termination sequence
15 cleavage site, and having a thymidine (or in the case of an mRNA, uracil) content of at least 80%. Functionally, thymidine-rich regions are currently believed to signal the polymerase complex transcribing the gene to pause prior to terminating transcription.

[66] The term "transfect," in all of its forms, refers to the transfer of a nucleic acid fragment into the genome of a host organism, resulting in genetically stable inheritance. Host
20 organisms containing the transformed nucleic acid fragments are referred to as "transgenic" organisms. Examples of methods of plant transformation include *Agrobacterium*-mediated transformation (De Blaere *et al.*, *Meth. Enzymol.*, 143:277 (1987)) and particle-accelerated or "gene gun" transformation technology (Klein *et al.*, *Nature* (London) 327:70-73 (1987); U.S. Pat. No. 4,945,050, incorporated herein by reference).

[67] "Transgenic" as used herein refers to any cell, cell line, tissue plant part or plant the
25 genotype of which has been altered by the presence of an exogenous coding region. Typically, the exogenous coding region was introduced into the genotype by a process of genetic engineering, or was introduced into the genotype of a parent cell or plant by such a process and is subsequently transferred to later generations by sexual crosses or asexual
30 propagation.

[68] The term "upstream element" refers to a region of nucleotide sequence that has within it the hexanucleotide TAYRTA or 2 or more repeats of TA, TG, or TA and TG, where the repeats are separated by 0 to 10 nucleotides. Functionally, upstream elements aid in

formation of the 3' termination sequence processing complex, and can modulate activity of the complex.

[69] The term "viable" refers to the ability of a biological component or system to function, live, develop, or germinate under favorable conditions.

5

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

[70] The present invention provides novel plant expression cassettes comprising non-plant 3' termination sequences, allowing for a greater degree of control over expression of the gene(s) contained within the cassette, whilst minimizing potential pitfalls associated with molecular interaction between homologous elements found in the expression cassette and the plant genome, such as molecular recombination and gene "silencing."

[71] Non-plant 3' termination sequences of the present invention are either isolated or engineered to possess particular sequence motifs found by the inventors to be necessary for gene function in plants. These motifs include a cleavage site, a positioning element and an upstream element, each element demanding particular sequence and location requirements be met if the 3' termination sequence is to be functional in plants.

[72] A general approach to isolating non-plant 3' termination sequences that are functional in plants involves first screening a gene sequence database, such as GENBANK, using the criteria noted above. Acceptable sequences isolated from this *in silico* screening of databases are then used to create PCR primers specific for the identified 3' termination sequence. The PCR primers are in turn used to amplify the 3' termination sequence from a suitable sequence library or from purified genomic DNA. Once isolated, the structure of the 3' termination sequence is checked for structural consistency with the polynucleotide expected from the sequence database search, and for functionality in biochemical assays, as described below.

[73] The *in silico* sequence search for putative 3' termination sequences having the desired criteria can be performed with any number of analysis algorithms available commercially and in the public domain, such as the BLAST or PILEUP programs mentioned earlier. One first uses the analysis program to locate a suitable 3' termination sequence positioning element. Suitable 3' termination sequence positioning elements are 6 nucleotides long, and have at least four nucleotides that are adenine residues. Suitable positioning elements must also be

located downstream from the coding sequence stop codon (UAA, UGA or UAG in frame with the coding sequence) for the gene containing the putative 3' termination sequence, and between 10 and 40 nucleotides upstream from a potential 3' termination sequence cleavage site (i.e., YA). Any putative 3' termination sequences lacking a positioning element meeting
5 these criteria are eliminated from the pool of putative sequences.

[74] Having limited the pool of putative 3' termination sequences to those having a suitable positioning element, the pool is then further limited by excluding all sequences lacking an upstream element as defined by the criteria of the present invention. This is accomplished by searching the pool for candidates having the sequence TAYRTA, or two or
10 more repeats of TA, TG, or TA and TG in any combination, where the repeats are contiguous, or separated by up to 10 nucleotides. To qualify as an upstream element, the sequence must also be located downstream from the stop codon of the coding sequence and no more than 250 nucleotides upstream from the 5' nucleotide of the positioning element. Any putative 3' termination sequences not having the upstream element nucleotide sequence
15 and location described above is discarded from the pool of 3' termination sequence candidates.

[75] 3' termination sequences remaining in the pool after discarding all of those sequences not meeting the criteria described in both of the previous two paragraphs are then tested for their functional characteristics in plants, as described in detail below.

20 [76] 3' termination sequences isolated in this manner will frequently be joined to a coding sequence, and possibly also to extraneous sequences 3' to the termination sequence of interest. These undesired sequences can be removed by methods common in the art. For example, their removal can be accomplished through cleavage with restriction endonucleases or a combination of restriction site engineering by site-directed mutagenesis combined with
25 endonuclease cleavage. The latter approach offers the additional benefit of engineering additional restriction sites into the termination sequence to ease subsequent cloning steps. This technique is described in detail in Example 1.

[77] By engineering these sequence motifs into other non-plant 3' termination sequences, it is possible to create novel non-plant 3' termination sequences that function in plants. The
30 invention therefore also provides methods for constructing non-plant 3' termination sequences that are functional in plants as well as methods for testing the functionality of expression cassettes comprising non-plant 3' termination sequences modified according to the present invention. These methods use recombinant DNA technology known in the art to

insert the common sequence motifs and where necessary to remove identified native motifs known to interfere with 3' termination sequence function in plants.

[78] The invention also provides novel expression cassettes incorporating non-plant 3' termination sequences modified as disclosed herein. These novel expression cassettes can be used to transform plant cells that in turn can be grown to transgenic plants. Transgenic plants transformed with the expression cassettes of the present invention display stable genetic properties, with those embodiments where the cassettes are integrated into the host genome displaying typical Mendelian genetic segregation in crosses with both wild type and other transgenic strains. Moreover, as a consequence of their heterologous nature, the non-plant 3' termination sequences of the present invention are much less likely to contribute to gene silencing of native transcripts, nor are they prone to undesired recombination with the host genome, both common problems with constructs comprising plant 3' termination sequences.

A. General recombinant methods

[79] This invention relies on routine techniques in the field of recombinant genetics. Basic texts disclosing the general methods of use in this invention include Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds., 1994).

[80] For nucleic acids, sizes are given in either kilobases (Kb) or base pairs (bp). These are estimates derived from agarose or acrylamide gel electrophoresis, from sequenced nucleic acids, or from published DNA sequences. For proteins, sizes are given in kilodaltons (kDa) or the number of amino acid residues. Proteins sizes are estimated from gel electrophoresis, from automated protein sequencing, from derived amino acid sequences, or from published protein sequences.

[81] Oligonucleotides that are not commercially available can be chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage & Caruthers, *Tetrahedron Letts.*, **22**:1859-1862 (1981), using an automated synthesizer, as described in Van Devanter *et. al.*, *Nucleic Acids Res.*, **12**:6159-6168 (1984). Purification of oligonucleotides is by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson & Reanier, *J. Chrom.*, **255**:137-149 (1983).

[82] One of skill in the art will recognize many ways of generating alterations in a given nucleic acid sequence. Such well-known methods include site-specific mutagenesis, PCR

amplification using degenerate oligonucleotides, exposure of cells containing the nucleic acid to mutagenic agents or radiation, chemical synthesis of a desired oligonucleotide (e.g., in conjunction with ligation and/or cloning to generate large nucleic acids) and other well-known techniques. See, e.g., Berger and Kimmel, *Guide to Molecular Cloning Techniques*, 5 *Methods in Enzymology*, Volume 152 Academic Press, Inc., San Diego, Calif. (Berger); Sambrook *et al.*, *Molecular Cloning--A Laboratory Manual* (2nd ed.) Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, N.Y., (Sambrook) (1989); and Current Protocols in Molecular Biology, F. M. Ausubel *et al.*, eds., *Current Protocols*, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1994 Supplement) 10 (Ausubel); Pirrung *et al.*, U.S. Pat. No. 5,143,854; and Fodor *et al.*, *Science*, **251**:767-77 (1991). Product information from manufacturers of biological reagents and experimental equipment also provide information useful in known biological methods. Such manufacturers include the SIGMA Chemical Company (Saint Louis, Mo.), R&D systems (Minneapolis, Minn.), Pharmacia LKB Biotechnology (Piscataway, N.J.), CLONTECH Laboratories, Inc. 15 (Palo Alto, Calif.), Chem Genes Corp., Aldrich Chemical Company (Milwaukee, Wis.), Glen Research, Inc., GIBCO BRL Life Technologies, Inc. (Gaithersburg, Md.), Fluka Chemica-Biochemika Analytika (Fluka Chemie AG, Buchs, Switzerland), and Applied Biosystems (Foster City, Calif.), as well as many other commercial sources known to one of skill. Using these techniques, it is possible to insert or delete, at will, a polynucleotide of any length into a 20 3' termination sequence nucleic acid described herein.

[83] For example, site-directed mutagenesis techniques are described in (Ling *et al.*, "Approaches to DNA mutagenesis: an overview", *Anal Biochem.*, **254**(2):157-178 (1997); Dale *et al.*, "In vitro mutagenesis", *Ann. Rev. Genet.*, **19**:423-462 (1996); Botstein & Shortle, "Strategies and applications of *in vitro* mutagenesis", *Science*, **229**:1193-1201 (1985); Carter, 25 "Site-directed mutagenesis", *Biochem. J.*, **237**:1-7 (1986); and Kunkel, "The efficiency of oligonucleotide directed mutagenesis" in *Nucleic Acids & Molecular Biology* (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin) (1987)); mutagenesis using uracil containing templates (Kunkel, "Rapid and efficient site-specific mutagenesis without phenotypic selection", *Proc. Natl. Acad. Sci. USA*, **82**:488-492 (1985); Kunkel *et al.*, "Rapid and efficient site-specific mutagenesis without phenotypic selection", *Methods in Enzymol.*, 30 **154**:367-382 (1987); and Bass *et al.* (1988); oligonucleotide-directed mutagenesis (*Methods in Enzymol.*, **100**:468-500 (1983); *Methods in Enzymol.*, **154**:329-350 (1987); Zoller & Smith, "Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment", *Nucleic Acids Res.*,

- 10:6487-6500 (1982); Zoller & Smith "Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors", *Methods in Enzymol.*, **100**:468-500 (1983); and Zoller & Smith, "Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template", *Methods in Enzymol.*, **154**:329-350 (1987));
- 5 Taylor *et al.* (1985) "The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA", *Nucl. Acids Res.*, **13**: 8765-8787 (1985); Nakamaye & Eckstein, "Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis", *Nucl. Acids Res.*, **14**:9679-9698 (1986); Sayers *et al.*, "Y-T Exonucleases in phosphorothioate-
- 10 based oligonucleotide-directed mutagenesis", *Nucl. Acids Res.*, **16**:791-802 (1988); and Sayers *et al.* (1988); mutagenesis using gapped duplex DNA (Kramer *et al.*, "The gapped duplex DNA approach to oligonucleotide-directed mutation construction", *Nucl. Acids Res.*, **12**:9441-9456 (1984); Kramer & Fritz, "Oligonucleotide-directed construction of mutations via gapped duplex DNA", *Methods in Enzymol.*, **154**:350-367 (1987); Kramer *et al.*,
- 15 "Improved enzymatic *in vitro* reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations", *Nucl. Acids Res.*, **16**:7207 (1988); and Fritz *et al.*, "Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions *in vitro*", *Nucl. Acids Res.*, **16**:6987-6999 (1988)).
- [84] Other techniques for altering DNA sequences include; Wells *et al.*, "Cassette
- 20 mutagenesis: an efficient method for generation of multiple mutations at defined sites"; *Gene*, **34**:315-323 (1985); and Grundstrom *et al.*, "Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis", *Nucl. Acids Res.*, **13**:3305-3316 (1985)), double-strand break repair (Mandecki, "Oligonucleotide-directed double-strand break repair in plasmids of *Escherichia coli*: a method for site-specific mutagenesis", *Proc. Natl. Acad. Sci. USA*, **83**:7177-7181 (1986); and Arnold, "Protein engineering for unusual environments", *Current Opinion in Biotechnology*, **4**:450-455 (1993)). Additional details on many of the above methods can be found in *Methods in Enzymology* Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.
- 25 The sequence of the cloned genes and synthetic oligonucleotides can be verified after cloning
- 30 using, e.g., the chain termination method for sequencing double-stranded templates of Wallace *et al.*, *Gene*, **16**:21-26 (1981).

B. Sources and methods for isolating 3' termination sequences

[85] In general, 3' termination sequences are isolated from genomic or cDNA libraries, or through amplification techniques using oligonucleotide primers and purified genomic DNA. In one embodiment of the present invention, non-plant 3' termination sequences that function in plants without alteration can be isolated from a variety of sources, by first identifying 3' ends of known non-plant genes that satisfy the selection criteria described herein. PCR primers can then be synthesized using sequence information from the selected 3' termination sequences and the primers used to amplify the non-plant 3' termination sequences from any suitable library or genomic DNA preparation. Examples of primers constructed using this technique are listed as SEQ ID NOS:4-9 and reproduced below. These primers were used to amplify 3' termination sequences from specific genes of the yeast *Saccharomyces cerevisiae*. The amplified 3' termination sequences are provided as SEQ ID NOS:1-3 and SEQ ID NOS 16-31.

Primer set for isolating the 3' termination sequence of SEQ ID NO:1:

15 SEQ ID NO:4 CAL1 (5)CE, coding strand termination sequence primer:
5'-GCGCGCGGAAGGAGGAAAGTGACTCCTTCGTTGC-3'

SEQ ID NO:5 CAL1 (3)NE, noncoding strand termination sequence primer:
5'-GGTACCTCATCATTTGGAGGTTCAAGTCATGGAG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:2:

20 SEQ ID NO:6 SPS1 (5)CE, coding strand termination sequence primer:
5'-GCGCGCAAGTCACAAGTAGTAGCGAGTTACAAC-3'

SEQ ID NO:7 SPS1 (3)NE, noncoding strand termination sequence primer:
5'-GGTACCTTGTAATATAACGAGGAAACGCAACTTATCC-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:3:

25 SEQ ID NO:8 KRE9 (5)CE, coding strand termination sequence primer:
KRE9-5CE: 5'-GCGCGCCATCCAAGAGATTGTCTTTGTCTGCAAG-3'

SEQ ID NO:9 KRE9 (3)NE, noncoding strand termination sequence primer:
5'-GGTACCAGCGAAACACCAGAGTTGACCCACAG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:16

30 SEQ ID NO:32 BDF1-5C1:
5'-CCTAGGTGAAGAAGAGTGACTGAATTTTG-3'

35 SEQ ID NO:33 BDF1-3N2:
5'-GGTACCGTAAATTTTGTGAGTTAGGTTG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:17

SEQ ID NO:34 CHS5-5C1:

5 5'-CCTAGGATTAATGGATGCCTTCAATGAG-3'

SEQ ID NO:35 CHS5-3N2:

5'-GGTACCTAGAATGTGTTTAGGGATAGTTG-3'

10 Primer set for isolating the 3' termination sequence of SEQ ID NO:18

SEQ ID NO:36 GSG1-5C1

5'-ACTAGTTAGCTTTATTGGATGACTTTATGG-3'

15 SEQ ID NO:37 GSG1-3N2:

5'-GGTACCAAGTGAAGATTTTGATTATACCAG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:19

20 SEQ ID NO:38 UBI2-5C1:

5'-CCTAGGAATTGCGTCCAAAGAAGAAGTTG-3'

SEQ ID NO:39 UBI2-3N2:

5'-GGTACCATATTACGTTGACGGGAGTTTTC-3'

25

Primer set for isolating the 3' termination sequence of SEQ ID NO:20

SEQ ID NO:40 IQG2-5C1:

5'-CCTAGGAGTCCACTCTTCACCTCGTCTTG-3'

30

SEQ ID NO:41 IQG2-3N2:

5'-GGTACCTTTTCCCTTTTGGTAGTCAC-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:21

35

SEQ ID NO:42 UBI3-5C1:

5'-CCTAGGTAAGTGTCATTCCGTCTACAAG-3'

SEQ ID NO:43 UBI3-3N2:

40 5'-GGTACCTACACATGTCATCGCAGTGGAC-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:22

SEQ ID NO:44 RPO2-5C1:

45 5'-CCTAGGTGATATAGTATATCATCCTTACG-3'

SEQ ID NO:45 RPO2-3N2:

5'-GGTACCCTTAGGTGATATCGAGC-3'

50 Primer set for isolating the 3' termination sequence of SEQ ID NO:23

SEQ ID NO:46 YEF3-5C1:

5'-CCTAGGTGATGCTTACGTTTCTTCTGACG-3'

5 SEQ ID NO:47 YEF3-3N2:

5'-GGTACCGTGGCAGTTACTTTATATAGAGTG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:24

10 SEQ ID NO:48 AOX-5C1:

5'-CCTAGGAGTTTGTAGCCTTAGACATGAC-3'

SEQ ID NO:49 AOX-3N2:

5'-GGTACCGGTAATTAACGACACCCTAGAGG-3'

15

Primer set for isolating the 3' termination sequence of SEQ ID NO:25

SEQ ID NO:50 NTBP-5C1:

5'-CCTAGGTCTAAAGAGTAGCAATTCTGATG-3'

20

SEQ ID NO:51 NTBP-3N2:

5'-GGTACCACTTTGACGGAACAGAGGATGGAAG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:26

25

SEQ ID NO:52 NHYM-5C1:

5'-CCTAGGACTGTTGCGTAGACATGAGC-3'

SEQ ID NO:53 NHYM-3N2:

30 5'-GGTACCAGTGCATTCCATGGATTCTG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:27

SEQ ID NO:54 NACT-5C1:

35 5'-CCTAGGATCGTCCACCGCAAGTGCTTC-3'

SEQ ID NO:55 NACT-3N2:

5'-GGTACCTGTATACTAGCAATACTGTAC-3'

40 Primer set for isolating the 3' termination sequence of SEQ ID NO:28

SEQ ID NO:10 hLaminLF:

5'-GGCGCGCCTAGGCCAAGCCCTGCGTCCAGCGAGC-3'

45 SEQ ID NO:11 hLaminLR:

5'-CGGGGTACCCCGAGTCAGCTTGTGCAACAGCGTCG-3'

Primer set for isolating the 3' termination sequence of SEQ ID NO:29

50 SEQ ID NO:56 hLaminSF:

5'-GGCGCGCCTAGGGAAGCCTGCACGCGGCAGTTC-3'

SEQ ID NO:57 hLaminSR:

5'-CGGGGTACCCCGGAATAAACTCAGAGGCAGAAC-3'

5

Primer set for isolating the 3' termination sequence of SEQ ID NO:30

SEQ ID NO:58 hC2F:

10 5'-GGCGCGCCTAGGCTAGCCATGGCCACTGAGCCCT-3'

SEQ ID NO:59 hC2:

5'-CGGGGTACCCCGCCAAGGCCAGCCCTACCTGGC-3'

15 Primer set for isolating the 3' termination sequence of SEQ ID NO:31

SEQ ID NO:60 UBQF:

5'-GGCGCGCCTAGGTGGCTGTTAATTCTTCAGTCATGGC-3'

20 SEQ ID NO:61 UBQR:

5'-CGGGGTACCCCGCCTAACTTGTAATGACTTAAACAGC-3'

[86] Alternatively, non-plant 3' termination sequences that are not functional in plants can
 25 serve as a backbone from which termination sequences that are functional in plants can be
 engineered. This is performed generally by removing or replacing sequence motifs present in
 the native non-plant 3' termination sequence that interfere with gene expression in plants, and
 adding the cis regulatory elements identified in the present invention as necessary
 components of a 3' termination sequence capable of functioning in plants.

30 *cDNA Libraries*

[87] Although cDNA libraries only provide information regarding the 3' termination
 sequence 5' to the polyadenylation/cleavage site, this information is frequently all that is
 required to construct a 3' termination sequence that is functional in plants. First, unlike 3'
 termination sequences of animal genes, plant gene 3' termination sequences do not have
 35 sequence elements necessary for correct 3' termination sequence processing downstream
 from the cleavage site. Second, transcription often terminates shortly after the polymerase
 transcribes the cleavage site. As a consequence, the nucleotide sequence 3' to the cleavage
 site is often much shorter and less important than the untranslated sequence 5' to the cleavage
 site.

[88] Recombinant or semi-synthetic 3' termination sequences can be constructed using the 3' termination sequence data from a cDNA library. This is accomplished, for example, by replacing the poly-A tail of the cDNA with either a nucleic acid located 3' to the cleavage site of a different 3' termination sequence, or by replacing the poly-A tail with a suitable synthetic nucleic acid. Alternatively, the cDNA nucleotide sequence information is valuable as a source of primers and probes for isolating full-length 3' termination sequences from genomic DNA or to search for the appropriate downstream sequences in various sequence databases such as GENBANK.

[89] Preparation of cDNA libraries can be performed by standard techniques well known in the art. Well known cDNA library construction techniques can be found for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1989). It will be readily apparent to those skilled in the art that libraries can be constructed from a variety of cell and viral types.

[90] In constructing a cDNA library, the mRNA is made into cDNA using reverse transcriptase, ligated into a recombinant vector, and transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known (*see, e.g.*, Gubler & Hoffman, *Gene*, **25**:263-269 (1983); Sambrook *et al.*, *supra*; Ausubel *et al.*, *supra*).

Genomic Libraries

[91] Genomic libraries provide a source for full-length 3' termination sequences. To construct a genomic library, the DNA is extracted from the tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage λ vectors. These vectors and phage are packaged *in vitro*. Recombinant phage are analyzed by plaque hybridization as described in Benton & Davis, *Science*, **196**:180-182 (1977). Colony hybridization is carried out as generally described in Grunstein *et al.*, *Proc. Natl. Acad. Sci. USA.*, **72**:3961-3965 (1975). See also, Gussow, D. and Clackson, T., *Nucl. Acids Res.*, **17**:4000 (1989).

Purified Genomic DNA

Genomic DNA can be easily purified from many sources using commercially available kits and following the manufacturer's instructions. Alternatively, genomic DNA preparations

from certain tissues and organisms can be purchased from various vendors or repositories such as the American Type Culture Collection (ATCC).

PCR Amplification

[92] As mentioned previously, polymerase chain reaction and other *in vitro* amplification methods are also useful in cloning 3' termination sequences. Examples include making nucleic acids to use as probes for detecting, in physiological samples, the presence of polynucleotides comprising a 3' termination sequence of the present invention, for nucleic acid sequencing, or other purposes (*see* U.S. Patents 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis *et al.*, eds, 1990)). Such methods can be used to amplify 3' termination sequences directly from genomic DNA, or from DNA libraries.

[93] Restriction endonuclease sites can also be incorporated into the primers and used in site-directed mutagenesis methods to create constructs for modification by insertion or deletion of nucleic acid(s). Sequences amplified by the PCR reaction can be purified from agarose gels and cloned into an appropriate construct for further amplification or other manipulation.

[94] PCR techniques include 5' and/or 3' RACE techniques, both being capable of generating a full-length 3' termination sequence from a suitable library (e.g., Frohman, *et al.*, *Proc. Natl. Acad. Sci. USA*, **85**:8998-9002 (1988)). The strategy involves using specific oligonucleotide primers for PCR amplification of DNA comprising a 3' termination sequence. These specific primers are designed through identification of nucleotide sequences either in the 3' termination sequence itself, and/or the vector comprising the 3' termination sequence.

Site-directed mutagenesis

[95] Site-directed mutagenesis may be used to modify non-plant 3' termination sequences to create 3' termination sequences that are functional in plants or to create restriction sites in a 3' termination sequence that can in turn be used to insert or delete specific nucleotide sequences necessary to create 3' termination sequences that are functional in plants from non-plant sources. The technique further provides a ready ability to prepare and test sequence variants by introducing one or more nucleotide sequence changes into the DNA.

[96] The technique of site-directed mutagenesis is generally well known in the field (see i.e., Adelman *et al.*, *DNA*, 2:183 (1983) and the references cited above). As initially developed, the technique typically employs a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage (Messing *et al.*, *Third Cleveland Symposium on Macromolecules and Recombinant DNA*, Ed: A. Walton, Elsevier, Amsterdam, (1981)). These phage are readily commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis, eliminating the step of transferring the gene of interest from a plasmid to a phage.

[97] In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded nucleic acid that includes within its sequence a 3' termination sequence. An oligonucleotide that is generally complimentary with the region of the 3' termination sequences but bearing nucleotide substitutions required to create a cis element necessary to render the 3' termination sequence functional in plants is then generated. Such oligonucleotides can be generated for example by the *de novo* (phosphoramidite) synthesis techniques noted above. This oligonucleotide is then annealed with the single-stranded nucleic acid comprising a 3' termination sequence, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. A heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered. Suitable techniques are also described in U.S. Pat. No. 4,888,286, incorporated herein by reference.

[98] The preparation of 3' termination sequence variants using site-directed mutagenesis is provided as a means of producing novel, potentially useful 3' termination sequences and is not meant to be limiting, as there are other ways in which 3' termination sequence variants may be obtained. For example, recombinant vectors comprising a 3' termination sequence may be treated with mutagenic agents to obtain sequence variants (see, e.g., the method described by Eichenlaub, *J. Bacteriol.*, 138:559-566 (1979)).

[99] Although the foregoing methods are suitable for use in mutagenesis, the use of site-directed primers in conjunction with the polymerase chain reaction (PCR) technique is

generally now preferred. Briefly, sequence information is modified by replacing directed nucleic acids in a non-plant 3' termination sequence by amplifying the non-plant 3' termination sequence with primers generally directed for the 3' termination sequence, but where at least one of the primers comprises the desired nucleotide substitutions resulting in
5 amplification of a 3' termination sequence containing the desired substitutions. Resulting reaction products should be examined by e.g., restriction mapping, electrophoresis and/or automated nucleotide sequencing to confirm the desired product is obtained.

Restriction endonucleases

[100] Although site-directed mutagenesis techniques allow for precise base alterations in a
10 nucleotide sequence, restriction endonucleases allow for larger pieces of polynucleotide to be inserted into or deleted from a 3' terminations sequence, either by using existing restriction sites or by first creating the necessary restriction sites by, for example, site-directed mutagenesis.

[101] In general, an endonuclease is an enzyme that is capable of breaking DNA into
15 smaller segments. An endonuclease is capable of attaching to a strand of DNA somewhere in the middle of the strand and breaking it. By comparison, an exonuclease removes nucleotides from the end of a strand of DNA. All of the endonucleases discussed herein are capable of breaking double-stranded DNA into segments. This may require the breakage of two types of bonds: (1) covalent bonds between phosphate groups and deoxyribose residues, and (2)
20 hydrogen bonds (A-T and C-G) which hold the two strands of DNA to each other.

[102] A "restriction endonuclease" breaks a segment of DNA at a precise sequence of bases. Over 100 different endonucleases are known, each of which is capable of cleaving DNA at specific sequences. See, e.g., Roberts, T. *et al.*, *Proc. Natl. Acad. Sci. USA*, **76**:760 (1979). All restriction endonucleases are sensitive to the sequence of bases. Some restriction
25 endonucleases create a "cohesive" end with a 5' overhang (i.e., the single-stranded "tail" has a 5' end rather than a 3' end). Cohesive ends can be useful in promoting desired ligations. For example, an EcoRI end is much more likely to anneal to another EcoRI end than to, for example, a HaeIII end.

[103] In addition, some endonucleases are sensitive to whether certain bases have been
30 methylated. For example, two endonucleases, MboI and Sau3a are capable of cleaving the DNA at the same sequence of bases, but MboI cannot cleave the sequence if an adenine residue present in the sequence is methylated (me-A). Sau3a can cleave this sequence,

regardless of whether either A is methylated. To some extent the methylation (and therefore the cleavage) of a plasmid may be controlled by replicating the plasmids in cells with desired methylation capabilities. An *E. coli* enzyme, DNA adenine methylase (dam), methylates the A residues that occur in GATC sequences. Strains of *E. coli* that do not contain the dam enzyme are designated as dam⁻ cells. Cells that contain dam are designated as dam⁺ cells.

[104] Several endonucleases are known which cleave different sequences, but create cohesive ends that are fully compatible with cohesive ends created by other endonucleases. For example, at least five different endonucleases create 5' GATC overhangs (MboI, Sau3a, BglII, BclI, and BamHI). A cohesive end created by any of the endonucleases will ligate preferentially to a cohesive end created by any of the other endonucleases. However, a ligation of cohesive ends created by different enzymes will in some cases create a new site that is not recognized by one or both of the restriction endonucleases creating the initial cohesive ends. For example, ligating a BglII end with a BamHI end will create a sequence that cannot be cleaved by either Bgl II or BamHI; however, it can be cleaved by MboI (unless methylated) or by Sau3a. Many other such examples exist and are known in the art.

C. Synthetic nucleic acid constructs

[105] As noted previously, semi-synthetic 3' termination sequences can easily be fashioned by replacing the poly-A tail of a suitable cDNA with a synthetic sequence derived from sequence 3' to the cleavage site of a second 3' termination sequence. (cf. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York, USA (1989)). Synthetic oligonucleotides can also be constructed for use as probes to isolate 3' termination sequences or for creating 3' termination sequences *de novo*. This *de novo* synthesis is generally performed using a series of overlapping oligonucleotides usually 40-120 bp in length, representing both the sense and non-sense (antisense) strands of the gene. These DNA fragments are then annealed, ligated and cloned. Alternatively, amplification techniques can be used with precise primers to amplify the whole 3' termination sequence, or a specific subsequence.

[106] Fragments corresponding to various parts of an entire 3' termination sequence, including the sequence of incorporated cis elements of the present invention, can optionally be from any source including different 3' termination sequences, and combined to form novel 3' termination sequences. Alternatively, cis elements from one 3' termination sequence may

be "swapped" into a different 3' termination sequence. See, e.g., Cunningham, *et al.*, *Science*, **243**:1330-1336 (1989); and O'Dowd, *et al.*, *J. Biol. Chem.*, **263**:15985-15992 (1988) for analogous techniques, each of which is incorporated herein by reference. Thus, new chimeric 3' termination sequences that are functional in plants will result from the functional linkage of the cis elements described in this invention in non-plant 3' termination sequences, with necessary deletion of interfering non-plant cis elements, the latter process again accomplished using standard recombinant DNA technology.

[107] Of course entirely novel 3' termination sequences can be constructed using sequence information from any number of sources, but preferably from sequence information relating to 3' termination sequences. Using the selection criteria disclosed herein, synthetic chimeric 3' termination sequence constructs can be created *de novo*, as discussed in more detail below.

[108] The 3' termination sequences of the invention, modified 3' termination sequences or hybrid 3' termination sequences may be prepared synthetically by established standard methods, e.g. the phosphoramidite method described by Beaucage and Caruthers, *Tetrahedron Letters*, **22**:1859-1869 (1981), or the method described by Matthes *et al.*, *EMBO J.*, **3**:801-805 (1984). According to the phosphoramidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in suitable vectors.

[109] Finally, as discussed briefly above, the portion of a 3' termination sequence upstream from the cleavage site of any expressed gene can be isolated from a suitable cDNA expression library. These partial 3' termination sequences can be used to create probes for isolation of full-length 3' termination sequences, or as templates that can be extended using synthetic oligonucleotides and standard PCR techniques known in the art and described above, to create full-length synthetic or semi-synthetic 3' termination sequences through ligation of heterologous oligonucleotides.

D. Molecular labels

[110] The particular label or detectable group used in the assays described herein is not a critical aspect of the invention, as long as it does not significantly interfere with binding of the nucleic acids or proteins used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable

by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS™); fluorescent dyes and techniques capable of monitoring the change in fluorescent intensity, wavelength shift, or fluorescent polarization (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like); radiolabels (*e.g.*, ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P); enzymes (*e.g.*, horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA); and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*). For exemplary methods for incorporating such labels, see U.S. Pat. Nos. 3,940,475; 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241.

[111] The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

[112] Non-radioactive labels are often attached by indirect means. Generally, a ligand (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecule (*e.g.*, streptavidin) that is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound.

[113] The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see*, U.S. Patent No. 4,391,904.

[114] Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated

with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

[115] Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Identifying non-plant 3' termination sequences that function in plants

[116] The present invention initially identifies four specific selection criteria for identifying non-plant 3' termination sequences capable of functioning in plants, namely;

[117] 1. The presence of a canonical positioning element downstream of a coding region stop codon

[118] 2. The presence of "T-rich regions" downstream of the positioning element

[119] 3. A bias for "A-rich" regions at or near the positioning element

[120] 4. The non-plant termination sequences have no homologous counterpart in the plant variety to be transformed.

[121] These four criteria are refined to greater precision to define a cleavage site comprising the sequence YA, a positioning element that is 6 bases long, at least 4 of which are adenine and located between 10 to 40 bases 5' of the cleavage site, and an upstream element that is located between 1 base and 250 bases 5' of the positioning element, and has a sequence comprising either TAYRTA or two or more repeats of TA, TG, or TA and TG where the repeats are separated by 0 to 10 bases. To ensure that the non-plant 3' termination sequence has no plant homologues, the additional limitation that the termination sequence must have at least 60% identity, sometimes at least 70% identity, occasionally at least 80% identity, or possibly at least 90% identity to a native fungal or native animal 3' termination sequence and less than 90% identity to a native plant 3' termination sequence was introduced.

[122] It is important to realize that while positioning elements and cleavage sites are present in a given 3' termination sequence in a 1:1 ratio, each positioning element/cleavage site pair may be accompanied by multiple upstream elements, with each upstream element meeting the criteria outlined above. The entire group of elements comprising a cleavage site, positioning element and one or more upstream elements is termed a 3' regulatory set. It is also important to recognize that the 3' termination sequences of the present invention may

comprise more than one 3' regulatory set, as is the case for plant 3' termination sequences generally. Additionally, experimental evidence (reviewed in Rothnie, *Plant Mol Biol* **32**:43-61 (1996)) has shown that when the original 3' end cleavage site is removed or mutated, cleavage can still occur at an appropriate position downstream of the functional positioning element, even in the absence of a suitable YA dinucleotide, although with less precision. Therefore, the absence or alteration of a known cleavage site does not necessarily preclude the functionality of a 3' regulatory set, as the termination sequence processing complex in plants may operate in some capacity in a distance-dependent manner based upon the positioning and upstream elements. This potential flexibility is recognized and is considered a variation of the criteria outlined above.

F. Obtaining non-plant 3' termination sequences that function in plants

[123] There are multiple ways of obtaining 3' termination sequences satisfying the criteria noted above and being functional in plants. For example, the 3' termination sequences can be identified from databases and the nucleic acid recovered from a DNA library by methods common to the art of molecular biology. Alternatively, the 3' termination sequences can be isolated from any non-plant source and engineered to meet the criteria for a 3' termination sequence functional in plants using the recombinant DNA techniques described above. Examples of using these selection criteria to identify non-plant 3' termination sequences capable of functioning in plants and in using the selection criteria for engineering novel 3' termination sequences that function in plants are detailed in the sections that follow.

Isolation of native non-plant 3' termination sequences that function in plants

[124] As noted above, a general approach to isolating non-plant 3' termination sequences that are functional in plants involves first screening a gene sequence database using the 3' termination motif criteria of the present invention. Acceptable sequences isolated from this *in silico* screening of databases are then used to create PCR primers specific for the identified 3' termination sequence. The PCR primers are in turn used to amplify the 3' termination sequence from a suitable sequence library or genomic DNA preparation. Once isolated, the structure of 3' termination sequence is checked for structural consistency with the polynucleotide expected from the sequence database search, and for functionality in biochemical assays, as described below.

[125] In an exemplary application, the 3' termination sequences of the CAL1, SPS1, and KRE9 genes were identified from *Saccharomyces cerevisiae* by *in silico* screening as potential candidates for testing. In the first step of the application, an *in silico* sequence search was performed by examining the GENBANK annotations of well-characterized yeast genes for which at least 350 bases of sequence downstream of the stop codon was provided. The search was confined to genes related to fungal biology (spore formation, chitin synthesis, etc.) and for which no plant counterparts are known or expected. The 3' sequences of these genes were then evaluated for the particular elements and properties outlined above. First, the 3' sequences were scanned for a positioning element 6 nucleotides long, where at least four nucleotides were adenine residues. The positioning elements also had to be located downstream from the coding sequence stop codon (UAA, UGA or UAG in frame with the coding sequence) of the gene and between 10 and 40 nucleotides upstream from a potential 3' termination sequence cleavage site (i.e., YA). Any yeast genes lacking a positioning element meeting these criteria were eliminated from the candidate pool of putative sequences.

[126] Having limited the pool of candidates to those nucleotide sequences having a suitable positioning element, the pool was further limited by excluding all sequences lacking an upstream element as defined by the criteria of the present invention. This was accomplished by searching the pool for candidates having the sequence TAYRTA, or two or more repeats of TA, TG, or TA and TG in any combination, where the repeats are contiguous, or separated by up to 10 nucleotides. To qualify as an upstream element, the sequences also had to be located downstream from the stop codon of the coding sequence and no more than 250 nucleotides upstream from the 5' nucleotide of the positioning element. Any yeast genes not having the upstream element nucleotide sequence and location described above were discarded from the pool of 3' termination sequence candidates.

[127] The remaining candidate nucleotide sequences were examined for T-rich regions around the putative positioning elements and cleavage sites. The CAL1, SPS1, and KRE9 gene 3' ends each have at least 2 copies of the classic animal positioning element (AATAAA), numerous nucleotide stretches with at least 4 out of 6 residues being adenine, and multiple T-rich regions. The 3' ends from these genes were chosen for further evaluation, although many more candidates were identified and the search was clearly not exhaustive. PCR primers were then constructed based on the published sequences of these 3 genes (see SEQ ID NOS: 4-9), and used to amplify each respective 3' termination sequence. Expression cassettes were then constructed comprising a promoter functional in plants operably linked with a reporter gene (beta-glucuronidase) or selectable marker gene

(neomycin phosphotransferase) which in turn was linked to one of the 3 isolated yeast 3' termination sequences. The expression cassettes were then used to transfect *Agrobacterium* sp., which were subsequently used to transform plant cells in transient or stable expression assays (see Figs. 1-3). Reporter gene expression was observed for each of the 3 yeast termination sequences described, at a level comparable to or greater than a control plant 3' end (from the *Arabidopsis* EF1a gene), and significantly greater than the reporter gene with no 3' termination sequence at all (Figure 1). Additionally, the 3' ends were sufficiently functional to allow nptII gene expression and selection of transformed roots and shoots on kanamycin-containing media (Figures 2 and 3). Therefore, the sequence criteria used to identify these yeast 3' termination sequences, and which share some common motifs with plant 3' termination sequences (see Figure 4), were sufficient to allow the identification of non-plant 3' termination sequence that are functional in plants:

[128] A second search with slightly modified criteria was conducted for additional *Saccharomyces cerevisiae* 3' ends that might also prove to be highly functional in plants. In this case, the candidate pool was not limited to genes related to fungal biology. Selected candidates from this *in silico* exercise include the 3' ends from GENBANK entries U18116, Z49198, U26674, X05729, X01474, X05730, X03128, and J05583.

[129] To extend the searching beyond *S. cerevisiae* 3' ends and into other fungal species, a limited *in silico* screen was carried out for *Aspergillus nidulans* 3' ends using the search parameters outlined above. Selected candidates from this screen include the 3' ends from GENBANK entries U28333, M22869, and AJ001157.

[130] A limited effort was made, using the criteria described above, to identify 3' ends from human genes that may be functional in plants. Possible candidates for isolation and *in planta* testing include the 3' ends from GENBANK entries X04803 and M94363.

25 *Engineering, non-plant 3' termination sequences to function in plants*

[131] While isolation of native non-plant 3' termination sequences that function in plants offers a direct way of obtaining the desired sequence material, engineering non-functional 3' termination sequences such that they will function in plants offers several additional benefits over using native sequences. First, engineered 3' termination sequences can be derived from any non-plant source. The only restrictions placed on the source material are that it is not derived from a plant and that it comprises the non-translated portion of a gene. This latter requirement is necessary as termination sequences are frequently several hundred to several

thousand bases long. Nucleic acids of these lengths are known to adopt complex secondary structures. In the case of nucleic acids comprising known 3' termination sequences, it is presumed that the secondary structure adopted will not inhibit gene expression in plants, at least after the sequence has been engineered to function in plants.

5 [132] As noted above, non-plant 3' termination sequences require at least one 3' regulatory group of elements to function in plants. To the extent that these elements are absent from the non-plant 3' termination sequence, they can be inserted using techniques well known in the art. For example, using the techniques described in detail above, restriction sites can be engineered into the non-plant 3' termination sequence at precise positions using site-directed
10 mutagenesis techniques, allowing for the insertion of the necessary sequence elements after restriction endonuclease digestion. Where a native sequence is positioned correctly and homologous to the regulatory element to be inserted, site-directed mutagenesis can be used to directly alter the native sequence and incorporate the desired regulatory element.

[133] Any non-plant source of genetic material can be used to obtain 3' termination
15 sequences suitable for modification according to the present invention. Generally 3' termination sequence material will be identified through database searches using the same search tools as described above for identifying non-plant 3' termination sequences that are functional in plants without modification. In the case of sequences sought for modification, however, the criteria applied is much less stringent than that described in the identification
20 procedure above.

[134] Sequences sought to be modified to function in plants must be from the 3' untranslated region of a gene capable of being expressed when in a native environment. As noted above, this requirement is necessary to limit the possibility of the termination sequence adopting an inhibitory secondary structure. By definition, this also means that the sequence
25 must be downstream (3') to the stop codon of the coding sequence of the gene. As a practical limitation, the sequence should also contain a cleavage site (YA) or, in the case of cDNA, terminate at the 3' end with a "Y" excluding any poly-dT (poly A) tail. In the case of a cDNA, or any other potential sequence lacking a complete cleavage site, a cleavage site and any additional 3' trailing sequences that may be added can be constructed by appending an
30 appropriate polynucleotide to the 3' terminus of the potential sequence lacking a complete cleavage site.

[135] As an example, a sequence suitable for engineering into a 3' termination sequence that is functional in plants can be obtained from a cDNA by constructing PCR primers for the cDNA and any 3' termination sequence having a complete cleavage site and trailing 3'

sequence. Using an overlapping primer that spans the cleavage site, a complete, chimeric 3' termination sequence can be created. The resulting chimeric 3' termination sequence will have a 5' end from the cDNA and a 3' end derived from the 3' termination sequence having a complete cleavage site and trailing 3' sequence. The 3' termination sequence having a
5 complete cleavage site and trailing 3' sequence can be from any source, including an entirely novel synthetic sequence.

[136] Once a termination sequence suitable for engineering has been isolated to serve as a platform for modifications, the 3' regulatory group members can be individually inserted into the 3' termination sequence. Alternatively, the entire 3' regulatory group can be inserted as a
10 unit, complete with nucleotide sequences intervening between the individual elements of the group to ensure proper orientation.

[137] An exemplary protocol for constructing heterologous 3' termination sequences functional in plants involves first cloning a non-plant 3' termination sequence into a standard ds-DNA plasmid. The plasmid is then converted to a ss-DNA by standard methods
15 (Maniatis *et al.*). The ss-DNA is annealed to 40-50 nucleotide DNA oligomers having base mismatches at the site(s) intended to be engineered to create restriction sites allowing for the directionally-controlled insertion of desired termination sequence elements of the present invention, or eliminate an interfering native element. The hybrid DNA is then converted to a closed ds-DNA plasmid vector by use of DNA polymerase and standard protocols. Plasmids
20 containing the desired alterations are next identified by restriction analysis following plasmid DNA isolation from *E. coli* strains transformed with the mutagenized DNA. The mutagenized DNA is isolated and subjected to restriction endonuclease cleavage, with a restriction enzyme capable of cleaving at the engineered restriction sites. The desired termination sequence elements, which can be entirely synthetic or derived from a biological
25 source (or combination of both) are then inserted into the non-plant 3' termination sequence. Analysis for structural correctness is confirmed by PCR and DNA sequencing. Genetic or biochemical tests are then carried out as detailed below to ensure the new construct in functional in plants.

[138] In some non-plant 3' termination sequences there exists sequence motifs that interfere
30 with gene expression in plants. This is particularly true in termination sequences isolated from animal sources that contain elements downstream from the termination sequence cleavage site not found in plants. These elements can be removed or replaced with neutral sequence using the recombinant techniques described above. As the sequence elements are

very short, (between 5 and 25 bases), neutral sequence can be determined through routine experimentation.

[139] It is contemplated that linker regions and the like can be used in constructing 3' termination sequences. Linker regions may be needed, for example, to correctly position regulatory elements.

Deletion analysis of 3' termination sequences

[140] Sequences within a 3' termination sequence that affect the functionality of the entire sequence in a given system may be determined by using deletion constructs analogous to those described by Sherri *et al.* for the determination of HSP70 intron alterations which impact transcription of genes operably linked thereto (see U.S. Pat. No. 5,593,874, hereby incorporated by reference). Briefly, several expression plasmids are constructed to contain a reporter gene operably linked to different candidate nucleotide sequences that are obtained either by restriction enzyme deletion of internal sequences of the 3' termination sequence, restriction enzyme truncation of sequences at the 5' and/or 3' termination sequence of the 3' termination sequence, or by the introduction of single nucleic acid base changes by site-directed PCR into the 3' termination sequence. Expression of the reporter gene by the deletion constructs is detected. Detection of expression of the reporter gene in a given deletion construct indicates that the candidate nucleotide sequence in that deletion construct comprises a functional 3' termination sequence. By quantifying the results, sequences inhibitory to 3' termination sequence function can be identified.

[141] Similarly, deletion analysis will also yield data allowing for the identification of nucleotide sequences necessary for, or enhancing 3' termination sequence function. Identified sequences can then be tested by incorporation into engineered 3' termination sequences at different locations relative to the cleavage site. By creating a number of constructs, each containing the necessary/enhancing nucleotide sequence at a different location in an engineered 3' termination sequence, the optimal nucleotide sequence and positioning of cis elements can be ascertained.

II. Constructing Expression Cassettes

[142] Expression cassettes of the present invention include both single gene expression cassettes and binary or multiple gene cassettes. Binary vector systems are described in

further detail in Gynheung An *et al.*, Binary Vectors, *Plant Molecular Biology Manual*, A3:1-19 (1980). Single gene expression cassettes invariably comprise a claimed 3' termination sequence. Generally, expression cassettes containing a single gene are constructed to test the functionality of the 3' termination sequence in the plant cell system being used. The gene in such systems, when expressed, displays a selectable marker trait that eases identification of a functional construct.

[143] In addition to a gene comprising a 3' termination sequence of the invention, multiple gene expression cassettes also contain a marker gene known to be functional in the plant expression system, preferably linked to a constitutive promoter. The nucleotide sequence encoding the marker is typically flanked on the 5' side by functional regulatory sequences, as described below, and flanked on the 3' side by a 3' termination sequence that is functional in a plant expression system. Exemplary 3' termination sequences that function in plants include the nopaline synthase 3' termination sequence, and the octopine T-DNA gene 7 3' termination sequence. Alternatively, the 3' termination sequence can be provided by the marker gene, if the 3' termination sequence of the gene is functional in the plant system being transformed.

[144] In the single gene expression cassette construct, the marker trait is used to identify both transformed cells and functional 3' termination sequences. The drawback of this strategy is that successfully transformed cells may nonetheless fail to display the marker trait because the 3' termination sequence being tested does not function in the plant expression system. Conversely, while the multiple gene expression cassette is designed to allow for identification of all successfully transformed cells, it does not readily indicate functionality of the 3' termination sequence being tested, unless the test 3' termination sequence is flanking a sequence for expression of a different marker trait than the accompanying marker gene known to be functional. Therefore, in both scenarios, a method of physically detecting the presence, and preferably the orientation, of the gene comprising the 3' termination sequence being tested is also desirable.

[145] Such physical techniques typically are known in the art and typically take the form of blotting assays, such as Northern and Southern blotting and the like, where oligonucleotide probes specific for the gene comprising the 3' termination sequence being tested are hybridized to RNA or DNA isolated from the transformed cell or its progeny. Using stringent hybridization conditions, only sequences of the isolated DNA derived from the expression cassette will be bound by the probes and identified. Another physical method involves sequencing the incorporated chimeric test gene. To facilitate the process, restriction

sites can be engineered into the expression cassette, allowing for ready isolation of the oligonucleotide to be sequenced.

A. Standard Methods

[146] Standard techniques for construction of the chimeric genes incorporated into the expression cassettes of the present invention are well known to those of ordinary skill in the art (Sambrook, J., Fritsch, E. F., and Maniatus, T., *Molecular Cloning, A Laboratory Manual* 2nd ed. (1989); Gelvin, S. B., Schilperoort, R. A., Varma, D. P. S., eds. *Plant Molecular Biology Manual* (1990)). A variety of strategies are available for ligating fragments of DNA, the choice of which depends on the nature of the termini of the DNA fragments. Preferred constructs will generally include a plant promoter. Suitable promoters include any constitutive, inducible, tissue or organ specific, or developmental stage specific promoter which can be expressed in the particular plant cell. Suitable such promoters are disclosed in Weising *et al.*, supra. The following is a partial representative list of promoters suitable for use herein: the CaMV 35S promoter (Odell, J. T., Nagy, F., Chua, N. H., *Nature*, **313**:810-812 (1985)), the CaMV 19S (Lawton, M. A., Tierney, M. A., Nakamura, I., Anderson, E., Komeda, Y., Dube, P., Hoffman, N., Fraley, R. T., Beachy, R. N., *Plant Mol. Biol.*, **9**:315-324 (1987)), nos (Ebert, P. R., Ha, S. B., An, G., *PNAS*, **84**:5745-5749 (1987)), Adh (Walker, J. C., Howard, E. A., Dennis, E. S., Peacock, W. J., *PNAS*, **84**:6624-6628 (1987)), sucrose synthase (Yang, N. S., Russell, D., *PNAS*, **87**:4144-4148 (1990)), α -tubulin, actin (Wang, Y., Zhang, W., Cao, J., McEhoy, D. and Ray Wu., *Molecular and Cellular Biology*, **12**:3399-3406 (1992)), cab (Sullivan, T. *et al.*, *Mol. Gen. Genet.*, **215**:431-440 (1989)), PEPCase (Hudspeth, R. L. and J. W. Grula., *Plant Mol. Biol.*, **12**:579-589 (1989)) or octopine synthase (OCS) promoters, the light-inducible promoter from the small subunit of ribulose bisphosphate carboxylase (Khoudi, *et al.*, *Gene*, **197**:343 (1997)) and the mannopine synthase (MAS) promoter (Velten *et al.*, *EMBO J.*, **3**:2723-2730 (1984); Velten & Schell, *Nucleic Acids Research*, **13**:6981-6998 (1985)). Tissue specific promoters such as root cell promoters (Zhang & Forde, *Science*, **279**:407 (1998); Keller, *et al.*, *The Plant Cell*, **3**(10):1051-1061 (1991); Conkling, M. A., Cheng, C. L., Yamamoto, Y. T., Goodman, H. M., *Plant Physiol.*, **93**:1203-1211 (1990)) and tissue specific enhancers (Fromm M. E., Taylor L. P., Walbot V., *Nature*, **312**:791-793 (1986)) are also contemplated to be particularly useful, as are inducible promoters such as ABA- and turgor-inducible promoters. Still other promoters are wound-inducible and typically direct transcription not just on wound induction, but also at the sites

of pathogen infection. Examples are described by Xu *et al.*, *Plant Mol. Biol.*, **22**:573-588 (1993); Logemann *et al.*, *Plant Cell*, **1**:151-158 (1989); and Firek *et al.*, *Plant Mol. Biol.*, **22**:129-142 (1993). The skilled artisan will recognize that the subject promoters and parts thereof, can be provided by other means, for example chemical or enzymatic synthesis

5 analogous to that described above for construction of 3' termination sequences.

[147] In the construction of heterologous promoter/structural gene combinations, the promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter
10 function and indeed may be necessary when the heterologous construct comprises elements from different genera.

[148] Several methods for isolation of promoters are known. For instance, the full length of a promoter sequence may be isolated if a portion of the promoter or the corresponding gene sequence is known. One skilled in the art will recognize that a variety of small or large insert
15 genomic DNA libraries may be screened using hybridization or polymerase chain reaction (PCR) technology to identify library clones containing the desired sequence. Typically, the desired sequence may be used as a hybridization probe to identify individual library clones containing the known sequence. Alternatively, PCR primers based on the known sequence may be designed and used in conjunction with other primers to amplify sequences adjacent to
20 the known DNA polynucleotide sequence. Library clones containing adjacent DNA sequences may thereby be identified. Restriction mapping and hybridization analysis of the resulting library clones' DNA inserts allows for identification of the DNA sequences adjacent to the known DNA polynucleotide sequence. Thus, promoters may be isolated if only a portion of a promoter sequence is known.

[149] The RNA produced by a DNA construct of the present invention also contains a 5' non-translated leader sequence. This sequence can be derived from the promoter selected to express the gene, and can be specifically modified so as to increase translation of the mRNA. The 5' non-translated regions can also be obtained from viral RNA's, from suitable eukaryotic genes, or from a synthetic gene sequence. The present invention is not limited to constructs,
30 as presented in the following examples. Rather, the non-translated leader sequence can be part of the 5' end of the non-translated region of the coding sequence for the virus coat protein, or part of the promoter sequence, or can be derived from an unrelated promoter or coding sequence. In any case, it is preferred that the sequence flanking the initiation site conform to the translational consensus sequence rules for enhanced translation initiation

reported by Kozak, M., *Nature*, **308**:241-246 (1984) and, of course, be functional in plants.

Regulatory elements such as Adh intron 1 (Callis, J. Fromm, M. and Walbot, V., *Genes and Develop.*, **1**:1183-1200 (1987)), sucrose synthase intron ("Mutagenesis of Cultured Cells" by P.J. King, *Cell Culture and Somatic Cell Genetics of Plants*, Chapter 61, vol. 1, By I.K.

- 5 Vasil, (Ed.) Academic Press, Inc., Orlando 1984, pp. 547-549) or TMV omega element (Gallie *et al.*, *Nucl. Acids Res.*, **15**:8693-8711 (1987)), may further be included where desired.

[150] In preparing the expression cassette, the various DNA sequences may normally be inserted or substituted into a bacterial plasmid. Any convenient plasmid may be employed, which will be characterized by having a bacterial replication system, a marker which allows
10 for selection in the bacterium and generally one or more unique, conveniently located restriction sites. These plasmids, referred to as vectors, may include such vectors as pACYC184, pACYC177, pBR322, pUC9, the particular plasmid being chosen based on the nature of the markers, the availability of convenient restriction sites, copy number, and the like. Thus, the sequence may be inserted into the vector at an appropriate restriction site(s),
15 the resulting plasmid used to transform the E. coli host, the E. coli grown in an appropriate nutrient medium and the cells harvested and lysed and the plasmid recovered. One then defines a strategy that allows for the stepwise combination of the different fragments.

[151] As necessary, the fragments may be modified by employing synthetic adapters, adding linkers, employing *in vitro* mutagenesis or primer repair to introduce specific changes
20 in the sequence, which may allow for the introduction of a desired restriction site, for removing superfluous base pairs, or the like. By appropriate strategies, one desires to minimize the number of manipulations required as well as the degree of selection required at each stage of manipulation. After each manipulation, the vector containing the manipulated DNA may be cloned, the clones containing the desired sequence isolated, and the vector
25 isolated and purified. As appropriate, hybridization, restriction mapping or sequencing may be employed at each stage to ensure the integrity and correctness of the sequence.

B. Coding sequences*non-plant genes*

[152] The coding region of genes comprising the expression cassettes of the present invention can be isolated from virtually any source, including but not limited to animal, viral, fungal and bacterial species, in addition to plants and genes normally associated with cellular organelles such as mitochondria and chloroplasts. Coding regions may also comprise chimeric genes and genes derived from ligating genomic regions of two or more gene sequences together to construct novel heterologous genes. Genomic sequences used in forming heterologous genes need not be isolated from a biological source, but may be designed in silico and produced chemically prior to incorporation into the expression cassette. Coding regions may be free of intronic sequences, or further comprise introns that are functionally recognized by the species to be transfected. Expression cassettes will typically include restriction enzyme sites at the 5' and 3' ends of the cassette to allow for easy insertion of genes into a pre-existing vector.

[153] By way of example, bacterial genes with insecticidal properties can be incorporated into the expression cassette. (e.g., de Maagd, R.A., *et al.*, "Bacillus thuringiensis toxin-mediated Insect Resistance in Plants", *Trends in Plant Sci.*, **4**(1):9-13 (1999); Fishhoff, D.A. and Bondish, K.S., "Insect tolerant transgenic tomato plants", *Bio/Technology*, **5**:807-813 (1987), U.S. Pat. No. 5,952,485 "Procedures and materials for Conferring Disease Resistance in Plants"). Other embodiments comprise antisense sequences capable of hybridizing to mRNA sequences thereby inducing "gene silencing", as applied for example to the control of fruit ripening. (U.S. Pat. No. 5,545,815). Still other embodiments provide methods for transfecting avian genes such as those for ovalbumin or α -actin, mammalian genes, such as human-EGF, or proteases such as trypsin and papain. Any coding construct of the present invention may be modified prior to transfection, either by molecular biological, chemical or other methods known in the art, to produce genes encoding proteins with enhanced or novel activities, targeting capabilities or extended biological half-lives, or simply to impart a codon set which is more efficiently utilized by the prospective transfected plant. An additional embodiment comprises entirely synthetic genes designed in silico from stored database sequences. Such synthetic genes may comprise functional domains from diverse molecules, imparting a unique set of properties to the transcribed protein.

Selectable marker genes

- [154] For purposes of screening successfully transfected cells and/or 3' termination sequences functional in plants, polynucleotides encoding selectable markers can be used in constructing the chimeric gene(s) of an expression cassette in the present invention.
- 5 Alternatively, the selectable marker may be carried on a separate piece of DNA and used in a co-transformation procedure with the expression cassette comprising the 3' termination sequence to be tested. Selectable markers are operably linked with appropriate regulatory sequences to enable expression in plants, in addition to the 3' termination sequence to be tested or a 3' termination sequence known to function in plants.
- 10 [155] Selectable marker genes can be isolated from any source and encode a variety of selectable traits. For example, one can employ antibiotic resistance genes, e.g., a kanamycin resistance gene or methotrexate resistance gene (DHFR). These genes are described in Haas and Dowding, "Aminoglycoside-Modifying Enzymes", *Meth. Enzymology*, **43**:611-628 (1975), and Bourouis *et al.*, *EMBO J.*, **2**:1099-1104 (1983). Additional genes include
- 15 chromogenic substrates; a luciferase (lux) coding region (Ow *et al.*, *Science*, **234**:856 (1986)), which allows for bioluminescence detection; an aequorin coding region (Prasher *et al.*, *Biochem. Biophys. Res. Comm.*, **126**:1259 (1985)), which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein coding region (Niedz *et al.*, *Plant Cell Reports*, **14**:403 (1995)); the chloramphenicol acetyl transferase gene (cat)
- 20 from Tn9 of *E. coli*, the beta-glucuronidase gene (gus) of the uidA locus of *E. coli*; the nptII gene which confers resistance to kanamycin (Messing & Vierra, *Gene*, **19**:259-268 (1982); and Bevan *et al.*, *Nature*, **304**:184-187 (1983)), the bar gene which confers resistance to the herbicide phosphinothricin (White *et al.*, *Nucl. Acids Res.*, **18**:1062 (1990); Spencer *et al.*, *Theor. Appl. Genet.*, **79**:625-631 (1990)), and the hph gene which confers resistance to the
- 25 antibiotic hygromycin (Blochliger and Diggelmann, *Mol. Cell. Biol.*, **4**:2929-2931 (1984)). Other markers are disclosed in K. Weising *et al.*, *Ann. Rev. of Genetics*, **22**:421 (1988). More recently, a number of selection systems have been developed which do not rely of selection for resistance to antibiotic or herbicide. These include the inducible isopentyl transferase system described by Kunkel *et al.*, *Nature Biotechnol.*, **17**:916-919 (1999).
- 30 [156] Expression of the selectable marker is determined at a suitable time after the DNA has been introduced into the recipient cells. A preferred assay entails the use of the *E. coli* beta-glucuronidase (GUS) gene (R. Jefferson *et al.*, *EMBO J.*, **16**:3901 (1987)). Plant cells transformed and expressing this gene will stain blue upon exposure to the substrate, 5-bromo-

4-chloro-3-indolyl- β -D-glucuronide (X-GLUC), and can also be used to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes CA *et al.*, *Methods Mol Biol*, **55**:121-131 (1995)). Thus, in one aspect, the present invention relates to an expression cassette that carries a construct encoding a GUS gene terminated by a 3' termination sequence of the present invention capable of introduction into the genome of, and expression in, a plant. This aspect of the invention is illustrated in Fig. 1, which illustrates the results of a test for functionality of yeast 3' ends in *Agrobacterium*-infiltrated *Nicotiana benthamiana* leaves. Plant binary expression cassettes were constructed containing the following genetic elements: the dMMV promoter linked to the beta-glucuronidase (GUS) reporter gene linked to a 3' end. The *Arabidopsis* EF1A 3' end served as the positive control plant 3' end, whereas an expression cassette with no 3' end served as the negative control. The vectors were transformed into *Agrobacterium tumefaciens* and used to infect *N. benthamiana* leaves. The infected leaves were stained for expression of the GUS reporter gene using a histochemical substrate, and then the green chlorophyll was removed from the leaves with ethanol. In the figure, the SPS1 and CAL1 yeast 3' ends appear to function as well or better than the plant EF1A 3' end, and the KRE9 3' end works slightly less well than the plant EF1A 3' end.

[157] Another aspect of the present invention relates to an expression cassette that carries a construct encoding an nptII gene terminated by a 3' termination sequence of the present invention capable of introduction into the genome of, and expression in, a plant. This aspect of the invention is illustrated in Figs. 2 and 3.

[158] Fig 2 depicts the functionality of yeast 3' termination sequences in the expression of kanamycin resistance in tobacco hairy roots. Plant binary vectors were constructed containing the following genetic elements: the dMMV promoter linked to the nptII selectable marker gene linked to a 3' termination sequence. The *Arabidopsis* EF1A 3' termination sequence served as the positive control plant 3' termination sequence. The vectors were transformed into *Agrobacterium rhizogenes* and used to infect tobacco leaf pieces. Successful transformation and root out-growth is an indication of the level of kanamycin resistance conferred by the selectable marker elements. The plates in the top row contain no kanamycin, whereas the plates in the bottom row contain 75 micrograms per milliliter kanamycin. Some variability in response is observed due to differences in the leaf explant material used for each transformation. Therefore, it is most informative to compare the number of root initials formed between the top and bottom plate for each construct.

[159] The CAL1 yeast 3' termination sequence appears to function about as well as the plant EF1A 3' termination sequence, the SPS and KRE9 3' termination sequences works reasonably well compared to the plant EF1A 3' termination sequence.

[160] Fig. 3 depicts the functionality of yeast 3' termination sequences in the expression of
5 kanamycin resistance in tobacco shoots. Plant binary vectors were constructed which contained the following genetic elements: the dMMV promoter linked to the nptII selectable marker gene linked to a 3' termination sequence. The *Arabidopsis* EF1A 3' termination sequence served as the positive control plant 3' termination sequence. The vectors were transformed into *Agrobacterium tumefaciens* and used to infect tobacco leaf pieces.
10 Successful transformation and shoot out-growth is an indication of the level of kanamycin resistance conferred by the selectable marker elements. The plates in the top row contain no kanamycin, whereas the plates in the bottom row contain 75 micrograms per milliliter kanamycin. Some variability in response is observed due to differences in the leaf explant material used for each transformation. Therefore, it is most informative to compare the
15 number of shoots formed between the top and bottom plate for each construct. Additional experiments confirm the general trends that are seen in the above photos.

[161] The CAL1, SPS, and KRE9 yeast 3' termination sequences appear to function about as well as the plant EF1A 3' termination sequence (poor explant material).

[162] In addition to providing expression cassettes for monitoring cellular transformation
20 and 3' termination sequence functionality in plants, the present invention also provides cassettes for the expression of any nucleic acid encoded trait, including antisense constructs for suppressing endogenous gene expression. Typically, however, the coding region will express a protein.

III. Identifying plant expression cassettes constructed with non-plant 3' termination 25 sequences

[163] To confirm the presence of the exogenous 3' termination sequences in plant cells, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays, including Southern and Northern blotting, and PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and
30 Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of a whole regenerated plant. Constructs may also be

engineered to ease isolation of all or part of the heterologous expression system, which can then be subjected to nucleic acid sequencing analysis.

A. In vitro assay systems

[164] Genomic DNA may be isolated from plant cell lines or any plant parts to determine the presence of the exogenous gene through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

[165] The presence of DNA elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique, discrete fragments of DNA are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a gene is present in a stable transformant, but does not prove integration of the introduced gene into the host cell genome. It is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that by using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced gene.

[166] Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique, specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition, it is possible through Southern hybridization to demonstrate the presence of introduced genes in high molecular weight DNA, i.e., confirm that the introduced gene has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR e.g., the presence of a gene, but also demonstrates integration into the genome and characterizes each individual transformant.

[167] It is contemplated that using the techniques of dot or slot blot hybridization, which are modifications of Southern hybridization techniques, one could obtain the same information that is derived from PCR, e.g., the presence of a gene.

[168] Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a transgene to progeny. The nonchimeric nature of the callus and the parental transformants (R_0) is demonstrated by germline transmission and identical Southern blot

hybridization patterns and intensities of the transforming DNA in callus, R₀ plants, and R₁ progeny that segregated for the transformed gene.

[169] Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA will only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced genes. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridization. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

B. Biochemical assay systems

[170] While Southern blotting and PCR may be used to detect the gene(s) in question, they do not provide information as to whether the gene is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced genes or evaluating the phenotypic changes brought about by their expression.

[171] Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique sequences and structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid

sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally used.

[172] Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed and may include assays for PAT enzymatic activity by following production of radiolabelled acetylated phosphinothricin from phosphinothricin and ^{14}C -acetyl CoA or for anthranilate synthase activity by following loss of fluorescence of anthranilate, to name two.

[173] Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological properties of the plant. Chemical composition may be altered by expression of genes encoding enzymes or storage proteins that have changes in amino acid composition and may be detected by amino acid analysis, or by enzymes which change starch quantity which may be analyzed by near infrared reflectance spectrometry. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays. An example is to evaluate resistance to antibiotics.

IV. Selection of transformants

[174] Once plant cells have been transformed with the expression cassette as described *supra*, it is necessary to identify and select cells that both contain the recombinant DNA and still retain sufficient regenerative capacity. There are two general approaches that have been found useful for accomplishing this. First, the transformed cells or plants regenerated therefrom can be screened for the presence of the recombinant DNA by various standard methods which could include assays for the expression of selectable markers or assessment of phenotypic effects of the recombinant DNA, if any, as described above. Alternatively, and preferably, when a selectable marker gene has been transmitted along with or as part of the recombinant DNA, those cells that have been transformed can be identified by the use of a selective agent to detect expression of the selectable marker gene, as exemplified in figs. 2 and 3.

V. Transgenic plants

[175] Transformed plant cells derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype such as increased seed mass. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans *et al.*, "Protoplasts Isolation and Culture", *Handbook of Plant Cell Culture*, pp. 124-176, Macmillan Publishing Company, New York (1983); and Binding, "Regeneration of Plants", *Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee *et al.*, *Ann. Rev. of Plant Phys.*, **38**:467-486 (1987).

A. Transfection techniques

[176] Expression cassettes of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the cassette may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. DNA can be stably incorporated into cells or can be transiently expressed using methods known in the art. Stably transfected cells can be prepared by transfecting cells with an expression vector having a selectable marker gene, and growing the transfected cells under conditions selective for cells expressing the marker gene. To prepare transient transfectants, cells are transfected with a reporter gene to monitor transfection efficiency. A review of the general techniques can be found in articles by Potrykus (*Annu. Rev. Plant Physiol. Plant Mol. Biol.*, **42**:205-225 (1991)) and Christou (*Agri-Food-Industry Hi-Tech* Mar./Apr. 17-27, 1994).

[177] DNA can also be introduced into plants by leaf disk transformation-regeneration procedures as described by Horsch *et al.*, *Science*, **227**:1229-1231 (1985), and other methods of transformation such as protoplast culture (Horsch *et al.*, *Science*, **223**:496 (1984); DeBlock *et al.*, *EMBO J.*, **2**:2143 (1984); Barton *et al.*, *Cell*, **32**:1033 (1983)) can also be used and are within the scope of this invention.

[178] Microinjection techniques are known in the art and thoroughly described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski *et al.*, *Embo. J.*, 3:2717-2722 (1984). Electroporation techniques are described in Fromm *et al.*, *Proc. Natl. Acad. Sci. USA*, 82:5824 (1985). Ballistic transformation techniques are described in Klein *et al.*, *Nature*, 327:70-73 (1987). Other methods are also available for the introduction of expression vectors into plant tissue, e.g., electroinjection (Nan *et al.*, In "*Biotechnology in Agriculture and Forestry*," Ed. Y. P. S. Bajaj, Springer-Verlag Berlin Heidelberg, 34:145-155 (1995); Griesbach, *HortScience*, 27:620 (1992)); fusion with liposomes, lysosomes, cells, minicells or other fusible lipid-surfaced bodies (Fraley *et al.*, *Proc. Natl. Acad. Sci. USA*, 79:1859-1863 (1982)); polyethylene glycol (Krens *et al.*, *Nature*, 296:72-74 (1982)); chemicals that increase free DNA uptake; transformation using virus, and the like.

[179] Alternatively, expression cassettes may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example, Horsch *et al.*, *Science*, 233:496-498 (1984), and Fraley *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:4803 (1983) and *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995).

[180] Alternatively, to enhance integration into the plant genome, terminal repeats of transposons may be used as borders in conjunction with a transposase. In this situation, expression of the transposase should be inducible, so that once the transcription construct is integrated into the genome, it should be relatively stably integrated and avoid further transposition.

[181] One of skill will recognize that after the expression cassette is stably incorporated into transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

[182] Using known procedures, one of skill can screen for plants of the invention by detecting the increase or decrease of marker mRNA or protein in transgenic plants or expression of marker traits by the transgenic plant. Alternative embodiments of the present invention allow for detection of target gene mRNA, protein or other trait, in which case the

optional marker genes can be omitted from the expression cassette. Methods for detecting and quantitation of mRNAs and proteins as well as screening assays for such traits as antibiotic resistance are well known in the art.

B. Site-directed integration

5 [183] Non-plant 3' termination sequences are particularly suited to applications requiring heterologous recombination between elements in the expression cassette and elements present in the host cell genome. Unlike commonly used plant 3' termination sequences, non-plant 3' termination sequences of the present invention have no homologous counterparts in the host cell genome. Consequently, non-plant 3' termination sequences are not prone to inadvertent
10 integration into the host cell genome by homologous recombination at the site of a 3' termination sequence homologue. Site-directed integration of the nucleic acid sequence of interest into the plant cell genome may be achieved by, for example, homologous recombination using *Agrobacterium*-derived sequences. Generally, plant cells are incubated with a strain of *Agrobacterium* which contains a targeting vector in which sequences that are
15 homologous to a DNA sequence inside the target locus are flanked by *Agrobacterium* transfer-DNA (T-DNA) sequences, as previously described (Offringa *et al.*, (1996), U.S. Patent No. 5,501,967, the entire contents of which are herein incorporated by reference). One of skill in the art knows that homologous recombination may be achieved using targeting vectors which contain sequences that are homologous to any part of the targeted plant gene,
20 whether belonging to the regulatory elements of the gene, or the coding regions of the gene. Homologous recombination may be achieved at any region of a plant gene so long as the nucleic acid sequence of regions flanking the site to be targeted is known.

[184] Where homologous recombination is desired, the targeting vector used may be of the replacement- or insertion-type (Offringa *et al.* (1996), *supra*). Replacement-type vectors
25 generally contain two regions which are homologous with the targeted genomic sequence and which flank a heterologous nucleic acid sequence, e.g., a selectable marker gene sequence. Replacement-type vectors result in the insertion of the selectable marker gene thereby disrupting the targeted gene. Insertion-type vectors contain a single region of homology with the targeted gene and result in the insertion of the entire targeting vector into the targeted
30 gene.

C. Producing transgenic Plants

[185] The transformed plant cell, usually in the form of a callus culture, leaf disk, explant or whole plant (via the vacuum infiltration method of Bechtold *et al.*, *C.R. Acad. Sci. Paris*, 316:1194-1199 (1993)) is regenerated into a complete transgenic plant by methods well-

5 known to one of ordinary skill in the art (e.g., Horsh *et al.*, 1985).

[186] Using these methods, virtually any gene, regardless of source, can be incorporated into the expression cassettes of the present invention for use in creating transgenic plants. The non-plant 3' termination sequences claimed herein are particularly useful for this purpose. In addition to failing to recombine with endogenous nucleotide sequences as noted above, the
10 lack of homology between the 3' termination sequences of the present invention and native plant 3' termination sequences also reduces the possibility of gene silencing through interference with transcripts comprising host 3' termination sequences. Similarly, because of the heterologous nature of the 3' termination sequences used in the claimed expression cassettes, transgenic plants created using these cassettes are genetically extremely stable and
15 the genetic traits encoded by the cassettes segregate in a predictable manner. Thus transgenic plants created using the present invention can be readily crossed with other stably transformed transgenic plants to create new transgenic plant strains having genomic stability equal to their parental plants.

[187] It may also be desirable to express a nucleic acid sequence that encodes an antisense
20 RNA that hybridizes with a genomic plant DNA sequence. For example, it may be of advantage to express antisense RNA that is specific for genomic plant DNA sequences that encode an enzyme whose activity is sought to be decreased. Examples of DNA sequences whose reduced expression may be desirable are known in the art including, but not limited to, the ethylene inducible sequences in fruits (U.S. Pat. No. 5,545,815, the entire contents of
25 which are herein incorporated by reference). Expression of antisense RNA that is homologous with these ethylene inducible sequences is useful in delaying fruit ripening and in increasing fruit firmness. Other DNA sequences whose expression may be desirably reduced include the ACC synthase gene, which encodes the enzyme that is the first and rate limiting step in ethylene biosynthesis. Nucleic acid sequences for this gene have been
30 described from a number of plant sources (e.g., Picton *et al.*, *The Plant J.*, 3:469-481 (1993); U.S. Pat. Nos. 5,365,015 and 5,723,766, the contents of both of which are herein incorporated by reference). Expression of antisense RNA that hybridizes with ACC synthase genomic sequences in plants may be desirable to delay fruit ripening.

[188] One of skill in the art knows that the antisense DNA segment to be introduced into the plant may include the full-length coding region of the targeted gene or a portion thereof.

Complete homology between the nucleotide sequences of the antisense RNA and the targeted genomic DNA is not required. Rather, antisense DNA sequences which encode antisense

5 RNA sequences that are partially homologous to a targeted genomic DNA sequence are contemplated to be within the scope of the invention so long as the antisense RNA sequences are capable of repressing expression of the target genomic DNA sequence.

[189] Also included within the scope of this invention are vectors that contain the same or different nucleic acid sequences under the transcriptional control of different 3' termination
10 sequences, and other sequences. Such vectors may be desirable to, for example, to control different levels of expression of different nucleic acid sequences of interest in plant tissues.

EXAMPLES

[190] The following examples are offered to illustrate, but not to limit the claimed invention.

15 **Example 1: Isolation and amplification of *Saccharomyces cerevisiae* CAL1 3' termination sequence.**

[191] Studies by the applicants have shown that at least three 3' termination sequences isolated from the yeast *Saccharomyces cerevisiae* function in plants as part of a heterologous expression cassette. The present example describes the isolation of one of these sequences by
20 PCR amplification.

[192] Oligonucleotide primers for PCR amplification were synthesized on an Applied Biosystems 394 DNA synthesizer using established phosphoramidite chemistry, precipitated with ethanol according to standard protocols, and used in the amplification reaction without further purification. The sequences of the synthetic primers were:

25

SEQ ID. NO:4 5'-GCGCGCGGAAGGAGGAAAGTGACTCCTTCGTTGC-3'
SEQ ID. NO:5 5'-GGTACCTCATCATTTGGAGGTTCAAGTCATGGAG-3'

30 A *Bss*H II restriction site (5'-GCGCGC-3') and an *Asp*718 I restriction site (5'-GGTACC-3') were incorporated at the ends of the SEQ ID. NO:4 and SEQ ID. NO:5 primers, respectively, to facilitate subcloning of the PCR-amplified 3' termination sequences into various plant expression cassettes.

[193] The CAL1 3' termination sequence (~485 bp) was amplified from the yeast chitin synthase 3 gene (GENBANK accession number X57300). PCR reactions were performed by mixing the primers with ~ 100 nanograms of *S. cerevisiae* genomic DNA prepared with a DNeasy™ Plant Mini Kit according to the manufacturer's (Qiagen) instructions. The primers
5 were added to a final concentration of 1 µM each to a mixture containing 10 mM TrisHCl (pH8.8), 25 mM KCl, 3.5 mM MgCl₂, 2.5 mM each deoxynucleoside triphosphate, 0.001% gelatin, 1.5 U AmpliTaq DNA Polymerase (Perkin-Elmer/Cetus), and the genomic DNA. Following 5 min denaturation at 95°C, the cycling conditions were 95 °C for 1 min, 45 °C for 1 min 30 s, and 72 °C for 30 s for 45 cycles. PCR products were T-A cloned into the pCR2.1-
10 Topo cloning vector according to the manufacturer's (Invitrogen) instructions. Cloning of the correct 3' end was confirmed by comparison of the Topo clone sequences to the sequence reported in GENBANK entry X57300.

Example 2: Construction of a recombinant expression cassette using the CAL1 3' termination sequence and testing non-plant 3' termination sequence function in plants.

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[194] This example describes the construction of a reporter expression cassette for testing 3' termination sequence functionality in plants. The reporter expression cassette comprises a dMMV promoter (Dey and Maita, Plant Mol Biol 40: 771-782 1999) operably linked to a β-glucuronidase (GUS) reporter gene containing a plant intron and a glycine-rich protein signal peptide secretion signal (Jefferson *et al.*, PCT WO99/13085). The Cal1 3' end was sub-cloned from the pCR2.1-Topo vector as a *Bss*H II-*Asp*718 I fragment into the *Bss*H II-*Asp*718 I sites of the plant binary vector pMAXY-3768 (Right border-dMMV promoter-GFP-[*Bss*H II]*Arabidopsis* EF1a 3' end[*Asp*718 I]-Left border). The "GUSplus + intron + SP" sequences
20 derived from pCAMBIA1305.2 were subcloned from pMAXY-3568 as an *Nco* I-*Asc* I fragment into the *Nco* I-*Bss*H II sites of the above vector to remove the GFP gene and insert the GUS reporter gene. The 3' termination sequence to be tested was operably linked to the GUS reporter sequence and located ~20 nucleotides downstream of the GUS stop codon. The completed expression cassette was then used to transform competent *Agrobacterium*
25
30 *tumefaciens* cells. Leaf tissue was infected with the recombinant *A. tumefaciens* using a

transformation procedure modified from Horsch *et al Science* 227:1229-1231 (1985), and the expression of β -glucuronidase is monitored by histochemical and fluorometric assays.

[195] In an exemplary construct, a *Saccharomyces cerevisiae* CAL1 3' termination sequence, amplified as described in example 1, was inserted into the reporter expression

5 cassette 3' to the reporter gene. Two control reporter expression cassette constructs were also produced: a positive control vector comprising an *Arabidopsis* EF1A 3' termination sequence, and a negative control lacking a 3' termination sequence of any type.

[196] All three vectors were transformed into *Agrobacterium tumefaciens* strain C58.

Successfully transfected *Agrobacterium* colonies were clonally selected based on the

10 Kanamycin resistance encoded by the vector nptIII gene. Briefly, *A. tumefaciens* transformed with each vector were plated on LB + KAN plates [per liter of medium: 10 g bacto-tryptone, 5 g bacto-yeast extract, 10 g NaCl, adjust pH to 7.0 with NaOH, 1.5% bacto-agar, plus 40 μ g/ml Kanamycin (PhytoTechnology Laboratories)] and allowed to incubate at 30°C for 48 hours. Two clones from each transformation were picked from the plates and suspended in

15 three ml of LB + KAN liquid media (as above without agar). The bacterial cultures were grown overnight at 30°C with rapid shaking (250 rpm).

[197] The saturated bacterial cultures were pelleted by centrifugation at 3500 rpm in an Eppendorf 5810 R centrifuge. The supernatants were decanted and the bacterial pellets resuspended in 3 ml of 10 mM Mg SO₄. Samples from each clonal selection were used to

20 infect separate, discrete areas on the same *Nicotiana benthamiana* leaf. Inoculation involved forcing between 100 to 250 microliters of bacterial suspension into the interstitial leaf spaces using a syringe (no needle) placed in direct contact with the underside of the leaf. The infected leaf, still attached to the plant, was allowed to incubate for 4 days at room temperature prior to staining with 5-bromo-4-chloro-3-indolyl-beta-D-glucuronide (X-

25 GLUC) according to the method described by R. Jefferson *et al.*, *EMBO J.*, 16, 3901 (1987). Chlorophyll was then removed from the tissue by treatment with 70% ethanol at room temperature for 2 days. The ethanol was repeatedly replaced with fresh stock as it turned green from the extracted chlorophyll. Test results are depicted in Table 2. Relative levels of GUS expression are depicted by the number of "+" present in each column.

30

TABLE 2. Functionality of *S. cerevisiae* CAL1 3' termination sequence in *Agrobacterium*-infected *Nicotiana Benthiana* leaves

	<u>3' Termination Sequence</u>	<u>GUS expression</u>
	EF1A	+++
5	CAL1	++++
	no 3' termination sequence	--

[198] From this inquiry, it is apparent that the *S. cerevisiae* CAL1 termination sequence is capable of supporting gene expression in plants, without overt modification.

10 [199] Comparative studies with *S. cerevisiae* SPS1 and KRE9 3' termination sequences also yielded positive results when incorporated into the reporter expression cassette as described in the method above. Expression of the reporter gene, however, appeared to be stronger for the construct comprising the CAL1 termination sequence than from constructs using either of the other two *S. cerevisiae* termination sequences (e.g., see fig. 1).

15

Example 3: Constructing a heterologous 3' termination sequence that is functional in plants from the 3' termination sequence from human genes.

20 [200] The following primer sets were used to PCR amplify 3' termination sequences from the genomic sequences corresponding to the indicated GENBANK accession numbers by using the PCR amplification method described in example 1 above.

	PRIMER NAME	PRIMER SEQUENCE	GENBANK REFERENCE
25	hLaminLF	5'- GGCGCGCCTAGGCCAAGCCCTGCGTCCAGCGAGC -3'	GENBANK AC#: M94363
	hLaminLR	5'- CGGGGTACCCCGAGTCAGCTTGTGCAACAGCGTCG -3'	
	hLaminSF	5'- GGCGCGCCTAGGGAAGCCTGCACGCGGCAGTTC -3'	GENBANK AC#: M94363
30	hLaminSR	5'- CGGGGTACCCCGGAATAAACTCAGAGGCAGAAC -3'	
	hC2F	5'- GGCGCGCCTAGGCTAGCCATGGCCACTGAGCCCT -3'	GENBANK AC#: L09708
35	hC2R	5'- CGGGGTACCCCGCCAAGGCCAGCCCTACCTGGC -3'	
	UBQF	5'- GGCGCGCCTAGGTGGCTGTAAATTCTTCAGTCATGGC -3'	GENBANK AC#: X04803
40	UBQR	5'- CGGGGTACCCCGCCTAACTTGTAATGACTTAAACAGC -3'	

[201] For the lamin gene, a long (L) and short (S) version of the 3' region were amplified.

The human 3' termination sequences were cloned into a plant binary vector and tested for activity in the leaf infiltration assay as described above.

- 5 GUS activity of four human 3' termination sequences in the *N. benthamiana* leaf infiltration assay.

3' end	Specific Activity (RFU/min/ug)	Relative Activity
C2	0.15	0.2
LAM S	0.21	0.2
UBQ	0.43	0.4
LAM L	0.46	0.4
EF1a	1.02	1
CAL1	1.66	1.6

- [202] All four of these human 3' termination sequences were weakly active and functional in the plant transient assay. The CAL1 3' termination sequence from *S. cerevisiae* (CAL1) and a 3' termination sequence from the *Arabidopsis* elongation factor 1a gene (EF1a) served as controls in this experiment.

15 **Example 4: Constructing a heterologous 3' termination sequence that is functional in plants from the 3' termination sequence of *Saccharomyces cerevisiae*.**

[203] The following primer sets were used to PCR amplify 3' termination sequences from the genomic sequences corresponding to the indicated GENBANK accession numbers by using the PCR amplification method described in example 1 above.

PRIMER NAME	PRIMER SEQUENCE	GENBANK REFERENCE
BDF1-5C1	5' - CCTAGGTGAAGAAGAGTGACTGAATTTTG -3'	GENBANK AC#: U18116
BDF1-3N2	5' - GGTACCGTAAATTTTGTGAGTTAGGTTG -3'	
CHS5-5C1	5' - CCTAGGATTAATGGATGCCTTCAATGAG -3'	GENBANK AC#: Z49198
CHS5-3N2	5' - GGTACCTAGAATGTGTTTAGGGATAGTTG -3'	
GSG1-5C1	5' - ACTAGTTAGCTTTATTGGATGACTTTATGG -3'	GENBANK AC#: U26674
GSG1-3N2	5' - GGTACCAAGTGAAGATTTTGATTATACCAG -3'	
UBI2-5C1	5' - CCTAGGAATTGCGTCCAAAGAAGAAGTTG -3'	GENBANK AC#: X05729
UBI2-3N2	5' - GGTACCATATTACGTTGACGGGAGTTTTC -3'	
IQG2-5C1	5' - CCTAGGAGTCCACTCTTCACCTCGTCTTG -3'	GENBANK AC#: X01474

IQG2-3N2 5' - GGTACCTTTTCCCTTTTGGTAGTCAC -3'

 UBI3-5C1 5' - CCTAGGTAAGTGTGTCATTCCGCTACAAG -3' GENBANK AC#: X05730

 5 UBI3-3N2 5' - GGTACCTACACATGTCATCGCAGTGGAC -3'

 RPO2-5C1 5' - CCTAGGTGATATAGTATATCATCCTTACG -3' GENBANK AC#: X03128

 RPO2-3N2 5' - GGTACCCCTTAGGTGATATCGAGC -3'

 10 YEF3-5C1 5' - CCTAGGTGATGCTTACGTTTCTTCTGACG -3' GENBANK AC#: J05583

 YEF3-3N2 5' - GGTACCGTGGCAGTTACTTTATATAGAGTG -3'

15 [204] The 3' termination sequences were cloned into the same plant binary test vector as described in example 2 above (Right border-dMMV promoter-GUS + intron + SP reporter gene-Left border).

20 [205] Functional analyses of the 3' termination sequences were conducted as described in Example 2 of the application (*Agrobacterium* infiltration into *N. benthamiana* leaves). Extracts were prepared from the infiltrated leaves and the GUS specific activity was determined using a quantitative fluorometric assay (essentially as described by Jefferson in Plant Molecular Biology Reporter 5(4): 387-405, 1987).

25 GUS activity of various *S. cerevisiae* 3' termination sequences in the *N. benthamiana* leaf infiltration assay.

3' end	Specific Activity (RFU/min/ug)	Relative activity
UBI3	0.18	0.3
BDF1	0.24	0.4
GSG1	0.42	0.7
CHS5	0.46	0.7
UBI2	0.50	0.8
IQG2	0.64	1.0
RPO2	0.97	1.6
YEF3	1.07	1.7
CAL1	0.40	0.7
nos 3'	0.61	1
EF1a	0.63	1

30 [206] This transient assay system is quite variable due to the nature of the procedure, so the relative activities should be viewed as a rough estimate. The key point to note is that all of the *S. cerevisiae* 3' termination sequences tested were active and functional in plants. Some of the 3' ends were relatively weak, such as UBI3 and BDF1, whereas others (i.e. RPO2 and

YEF3) had activity greater than the control plant 3' ends. 3' termination sequences from the *Agrobacterium* nopaline synthase gene (nos 3') and the *Arabidopsis* elongation factor 1a gene (EF1a) were used as controls in this experiment.

5

Example 5: Constructing a heterologous 3' termination sequence that is functional in plants from the 3' termination sequence of *Aspergillus nidulans*.

[207] The following primer sets were used to PCR amplify 3' termination sequences from the genomic sequences corresponding to the indicated GENBANK accession numbers by using the PCR amplification method described in example 1 above.

	PRIMER NAME	PRIMER SEQUENCE	GENBANK REFERENCE
15	AOX-5C1	5' - CCTAGGAGTTGTAGCCTTAGACATGAC -3'	pPICZα (Invitrogen)
	AOX-3N2	5' - GGTACCGTAATTAACGACACCCTAGAGG -3'	

	NTBP-5C1	5' - CCTAGGTCTAAAGAGTAGCAATTCTGATG -3'	GENBANK AC#: U28333
20	NTBP-3N2	5' - GGTACCACTTTGACGGAACAGAGGATGGAAG -3'	

	NHYM-5C1	5' - CCTAGGACTGTTGCGTAGACATGAGC -3'	GENBANK AC#: AJ001157
25	NHYM-3N2	5' - GGTACCAGTGCATTCCATGGATTTCG -3'	

	NACT-5C1	5' - CCTAGGATCGTCCACCGCAAGTGCTTC -3'	GENBANK AC#: M22869
	NACT-3N2	5' - GGTACCTGTATACTAGCAATACTGTAC -3'	
30	-----		

[208] The *Aspergillus* and *Pichia* 3' termination sequences were cloned into a plant binary vector and tested for activity in the leaf infiltration assay as described above.

35 GUS activity of three *A. nidulans* 3' termination sequences and one *P. pastoris* 3' termination sequence in the *N. benthamiana* leaf infiltration assay.

3' end	Specific Activity (RFU/min/ug)	Relative Activity
NHYM	0.21	0.4
NACT	0.21	0.4
NTBP	0.34	0.6
AOX	0.70	1.3
nos 3'	0.54	1
CAL1	0.81	1.5
EF1a	1.39	2.6

[209] All four of these fungal 3' termination sequences were active and functional to various degrees in the plant transient assay. A 3' termination sequence from the *Agrobacterium* nopaline synthase gene (nos 3') and a 3' termination sequence from the *Arabidopsis* elongation factor 1a gene (EF1a) served as controls in this experiment.

5

Example 6: Constructing a synthetic, heterologous 3' termination sequence that is functional in plants using oligonucleotide primers.

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[210] This example provides a conceptual framework for building synthetic or semi-synthetic 3' termination sequences using oligonucleotide primers. It is meant to exemplify, but not to limit, the possible approaches that could be used to construct non-plant 3' termination sequences that have functionality in plants. As a first step in creating an upstream element, the following primers are designed and annealed together:

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SEQ ID NO:62 Up1CA 5' - AATTCTATGTATGTGTGTTTGTGTGTGTG -3'
 SEQ ID NO:63 Up2NA 5' - AATTCACACACACAAACACACACATACATAG -3'

[211] When these 2 primers (containing a TAYRTA sequence and multiple TG repeats) anneal together, the double-stranded oligonucleotide pair forms EcoR I-compatible sticky ends that can be ligated into the EcoR I site of pBSSK+ (Stratagene). In the next step, a positioning element and downstream cleavage site are created by designing and annealing the following primers:

20

25

SEQ ID NO:64 PECS1CA 5' - AGCTTAATAAATAAATATTTCTCTATCTTTAAAGGCAC -3'
 SEQ ID NO:65 PECS2NA 5' - TCGAGTGCCTTTAAAGATAGAGAAATATTTATTATTAA -3'

[212] When these 2 primers (containing 2 copies of AATAAA followed by YA's at 10-40 nucleotides downstream) anneal together, the double-stranded oligonucleotide pair forms one *Hind* III-compatible end and one *Xho* I-compatible end that can be ligated into the *Hind* III and *Xho* I sites of the above pBSSK+ vector containing the engineered upstream region. Finally, additional spacer DNA can be added downstream of the cleavage site(s) by PCR amplification of a T-rich region from any yeast gene 3' end. The primers used for this purpose would be designed to introduce *Xho* I and *Kpn* I restriction sites at the 5' and 3' ends of the amplified nucleic acid, respectively. This spacer fragment would be subcloned into the

35

Xho I and *Kpn* I sites of the above pBSSK+ vector containing the engineered upstream region plus positioning element(s) and cleavage site(s). The final, assembled 3' regulatory set would then be subcloned as a *Bss*H II to *Kpn* I fragment into the *Bss*H II to *Asp* 718 I sites of a plant expression vector for *in planta* testing as described above in Example 2.

- 5 **[213]** Vectors used to clone and express the 3' termination sequences of the present invention are derivatives of commercially available plasmids such as pCR2.1-Topo (Invitrogen, San Diego, Calif.), pBSSK+ (Stratagene, La Jolla, Calif.) and pBI121 (Clontech, Palo Alto, Calif.).

- 10 **[214]** It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.